

#### STIC Database Tracking Number: 137736

TO: Bao-Qun Li

Location: rem/3d24/3c18

Art Unit: 1648

Wednesday, November 17, 2004 Case Serial Number: 10/784537 From: Paul Schulwitz

**Location: Biotech-Chem Library** 

**REM-1A65** 

Phone: (571)272-2527

paul.schulwitz@uspto.gov

#### Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



Aar19363 homo

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

Result Š.

Title: Perfect score:

Sequence:

OM protein

Run on:

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Q9vskl drosophila
Q965s2 homo sapien
Q99135 homo sapien
Q90827 gallus gall
Q9fkn9 arabidopsis
P98092 bombyx mori
Q8axc3 xenopus lae
P22652 gallid herp
P22653 gallid herp
Q77mr7 meleagrid h
Aaff6780 turkey he
Aag44238 turkey he
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MEDLINE-21595285; PubMed=11759840;

MEDLINE-21595285; PubMed=11759840;

MEDLINE-21595285; PubMed=11759840;

Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Makazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.,

"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213 (2001).

R PIR; AE2094; AE2094.

R GO; GO:0005506; F:iron ion binding; IEA.

GO; GO:000518; P:electron transport; IEA.

R GO; GO:000518; P:electron transport; IEA.

R PRINTS; PRO0137; Fer4; 1.

R PROSITE; PRO0137; Fer4; 1.

R PROSITE; PRO0158; #FER4S FERENDXIN.

R PROSITE; PRO0158; #FER4S FERENDXIN.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PMM1560;
Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Last annotation update)
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Pred. No. 12;
0; Mismatches
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Q8AXC3
UL45 GAHVB
                    Q9VSK1
Q96JS2
NEL2 HUMAN
NEL_CHICK
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Q77MR7
AAF66780
AAG14238
AAS01688
  AAR19363
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77.8%;
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OrderedLocusNames=alr2308;
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Matches 7; Conservative
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Q8den3 vibrio vuln
Q7q460 anopheles g
Q8hxe2 macaca fasc
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Q7uzu5 prochloroco
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                                                                                                                                                          November 16, 2004, 14:14:16; Search time 53.6604 Seconds (without alignments) 96.503 Million cell updates/sec
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Q6s518
Q8iyw3
                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                             1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
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07RDG3
07RDG3
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06UXQ3
06GC16
085A69
06GC16
06GC16
06GC16
06GV13
09SZZO
099WD0
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Q7UZU5
Q8GL14
Q61KM6
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Gapop 10.0 , Gapext 0.5
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Q8DEN3
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2: uniprot_trembl:*
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seq length: 200000000
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Gaps

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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;

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                                                                                                                         ORFNames=HDC12057;
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                                                            Q6IKM6;
05-JUL-2004
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MEDLINE=22450571; PubMed=12562813;

Katayama M., Kondo T., Xiong J., Golden S.S.;

*IdpA encodes an irror-sulfur protein involved in light-dependent modulation of the circadian period in the cyanobacterium Synechococcus elongatus PCC 7942.";

J. Bacteriol. 185:1415-1422 (2003).

EMBL, AV136759; AAN06910.1; -.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:00056118; P:electron transporter iEA.

GO; GO:00050118; P:electron transport. IEA.

GO; GO:00050118; P:electron transport. IEA.

Fign. PP00037; Ferty. IEA.

PFam: PP00037; Ferty.
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MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
Rocap G., Larimer Fw., Lamerdin J.E., Malfatti S., Chain P.,
Rocap G., Larimer Fw., Coleman M.D., Hauser L., Hess W.R.,
Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation."
Nature 424:1042-1047(2003).
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PROSTIE; PSO0198; 4FE4SF FERREDOXIN; 1.
4FE-4S; Iron-sulfir; Metal-binding.
SEQUENCE 352 AA; 37865 MW; 33614612158F2936 CRC64;
                                                                                                                                                                                                                                                                                          336 AA; 37282 MW; CBC53CA6F8A27AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches 7; Conservative
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                        NCBI_TaxID=59919;
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Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C., Pellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J., Paro R.; An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5:R3-R3(2003).

-! MISCELLANBOUG: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.

EMBL, BK002340; DAA03846.1; ...
SEQUENCE 146 AA; 15612 MW; D23DCA44DCFAARC5 CRC64;
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                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Jang H., Cai J., Izumiya Y., Murakami Y., Mochizuki M., Song Lee Y., Kai C., Takahashi E., Mikami T.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB012572; BAA32581.1;
EMBL, AB024414; BAA82941.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.7%; Score 42; DB 2; Length 146; 75.0%; Pred. No. 29;
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Incerpro; IPR00981; Varicello_UL45.
Pfan; PF07144; Varicello_UL45; 1.
SEQUENCE 210 AA; 2303@ MW; 6ED41E888FC10E53 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=36353;
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05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Virion protein (UL45 product homolog).
Name=UL45; Synonyms=ORF 53;
                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
PRELIMINARY;
                                                                                     (TrEMBLrel.
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; 0

Gaps

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Length 348;

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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annoctation update)
Hematological and neurological expressed protein 1B (Hematological and neurological expressed gree 1-like protein variant b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                020000;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-UNV-1996 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein P35AS.4.
ORFNames=P35A5.4;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.9%; Score 41; DB 2; Length 181; 55.6%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang J., Zhou G., Yu L., Zhao S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7322169; AAPB33811; -.
EMBL; AF348672; AAPB3362.1; -.
SEQUENCE 181 AA; 19916 MW; FF644A114DE28850 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Zhou G., Guo J., Yu L.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases,
 DB 2;
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               65;
                             2; Mismatches
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 Score 42;
Pred. No. 6
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
73.7%;
55.6%;
                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 05-JUL-2004 (TrEMBLrel. 27,
Query Match 73.7
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                       Name=HN1; Synonyms=HN1A;
Homo sapiens (Human).
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                                                                          107 CPRPCQRVC 115
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152 CPERCRSVC 160
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                                                            1 CPRECESIC
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Leimbach D.;
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Q20000
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MEDLINE-2225697; PubMed=12917641; DOI=10.1038/nature01943;

MEDLINE-2225697; PubMed=12917641; DOI=10.1038/nature01943;

A Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,

Chain P., Lamerdin J.E., Partensky F.W., McCarren J.,

A Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

The genome of a motile marine Synechococcus.";

Nature 424:1037-1042(2003)

R GO; GO:0005506; Pelectron transporter activity; IEA.

R GO; GO:0005506; Pelectron transporter activity; IEA.

R GO; GO:0005506; Pelectron transport; IEA.

R GO; GO:000518; Pelectron transport; IEA.

R HIGEPROJ : 4Fe4S_FERREDOXIN; I.
                               Gaps
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"A Complete Genomic DNA Sequence of Marek's Disease Virus Type 2,
Strain HPRS24.";
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Score 42; DB 2; Length 210;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2; Length 210;
Pred. No. 41;
1; Mismatches 2; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Curr. Top. Microbiol. Immunol. 0:0-0(2000).

EMBL; AB049735; BAB16555.1; -.

InterPro; IPR09817; Varicello UL45.

Pfam; PF07144; Varicello UL45; 1.

SEQUENCE 210 AA; 23038 MW; 6ED41E988FC10E53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                     Gallid herpesvirus 3.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                             1; Mismatches
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66.78;
73.78;
66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                             6; Conservative
                                                                                                                                                                  PRELIMINARY;
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161 CPRTCTAIC 169
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=35250;
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                                                                                                                                                                                                                                           UL45 protein.
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Q782P9;
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Q7U4K2;
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                               Matches
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strain 1.";
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                                                                                                      Q7MBG7
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                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Chockenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.N. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002)
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                 ;
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BMBL; AABLO1001737; EAA17486.1; -.

GO; GO:0003870; F:5-aminolevulinate synthase activity; IEA.

GO; GO:0000481; F:1-aminolevulinate synthase activity; IEA.

GO; GO:0006783; P:heme biosynthesis; IEA.

R GO; GO:0006783; P:heme biosynthesis; IEA.

R InterPro; IPR001961; Saminolev synth.

R InterPro; IPR001999; Ala synthase.

R InterPro; IPR001997; Aminotrans I/II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 631;
                                                                                                                                                                                                                                             Score 41; DB 2; Length 273;
Pred. No. 76;
4; Mismatches 1; Indels
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Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; U46675; AABS2645.1; -.
PIR; T16246; T16246.
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Pfam; PF00155; Aminotran 1 2; 1.
TIGRFAMS; TIGR01821; Saminolev synth; 1.
PROSITE; PS00599; AA TRANSFER CLASS 2; UNKNOWN 1.
SEQUENCE 631 AA; 72951 NW; D266BDE7255CD842 CRC64;
                                                                                              WormPep; F35A5.4; CE04488.
InterPro; IPR003341; DUF139.
Pfam; PF02363; C_tripleX; 9.
Hypochetical protein:
SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-21004 (TrEMBLrel. 26, Last annotation update)
Delta-aminolevulinic acid synthetase.
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Best Local Similarity 44.4%,
A; Conservative
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les 5; Conservative
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146 CPQQCQPVC 154
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STRAIN-ESM2 1740;

MEDLINE-22882897; PubMed-14500908;

MEDLINE-22882897; PubMed-14500908;

MEDLINE-22882897; PubMed-14500908;

MEDLINE-22882897; PubMed-14500908;

MEDLINE-22882897; PubMed-14500908;

Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Lider B.C.;

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Meyer F., Meyer M., Meyer M.
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                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Wolinella.
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BEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Iudwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.9%; Score 41; DB 2; Length 649; 66.7%; Pred. No. 1.7e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72557 MW; CCA1E7589E36650D CRC64;
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Last annotation update)
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EMBL; BX294137; CAD72749.1; -.
InterPro; IPR004619; Baf.
Pfam; PF03309; Bvg_acc_factor; 1.
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649 AA
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Name=FDHB; OrderedLocusNames=WS0477;
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                                                             01-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last seq 01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Oxidoreductase. SEQUENCE 649 AA; 72557 MW; CCJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00070; Pyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00469; PNDRDTASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=RB2632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                               Wolinella succinogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=844;
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NCBI_TaxID=9606;
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Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
Chow B., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watenabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                                Score 40; DB 2; Length 295;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.2%; Score 40; DB 2; Length 387; 55.6%; Pred. No. 1.5e+02; ive 2; Mismatches 2; Indels
TIGRFAMs; TIGR00671; baf; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 295 AA; 31445 MW; 430B95673709B7A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              05-JTL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bioinformatics assessment.";
Genome Res. 13:2565-2270(2003).
EMBL; AY358250; AAQ88617.1; -.
InterPro; IPR0011036; PH related.
InterPro; IPR006019; PID domain.
InterPro; IPR006020; PTB PID.
InterPro; IPR000980; SH2.
                                                                                     70.2%;
85.7%;
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PRINTS; PR00629; SHCPIDOMAIN.
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(TrEMBLrel. 27, L
(TrEMBLrel. 27, L
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                                                               Query Match
Best Local Similarity 85...
6; Conservative
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PROSITE; PS01179; PID; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 387 AA; 42782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000093; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00640; PID; 1.
Pfam; PF00017; SH2; 1.
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89 RECESVC 95
                                                                                                                                                                        3 RECESIC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames=UNQ6438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ88617;
02-MAR-2004
02-MAR-2004
02-MAR-2004
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ID AAQ8
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PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matenno A., Muzaki A., Nakazaki N., Narno K., Okumura Simpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
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"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6603. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2.153-166(1995).
EMBL; D64006; BAA10799.1; -.
PIR; S75952.
HSSP, P00193; 1DUR.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics Assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AX358250; AAQ88617.1; -.
SEQUENCE 387 AA; 42782 MW; 558D4E2167B69AF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sll0031 protein.
OrderedLocusNames=sll0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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Homo sapiens (Human)
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Best Local Similarity
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DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR001450; 4Fe45_ferredoxin.

DR Pfam; PF00037; Fer4;

DR PRO3TTE; PR00353; 4FE45FEDOXIN.

DR PROSTTE; P$00198; 4FE45 FERREDOXIN; 1.

KW 4Fe-45; Complete proteome; Iron; Iron-sulfur; Metal-binding.

SQ SEQUENCE 395 AA; 43410 MW; 077421437A6B0DC0 CRC64;

Query Match

Query Match

A0.2%; Score 40; DB 2; Length 395;

Best Local Similarity 55.6%; Pred. NO: 1.6e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 16, 2004, 14:29:46 Job time : 55.6604 secs

1 CPRECESIC 9 ||| | :| 131 CPRPCAQVC 139

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ABG60452 standard; peptide; 13 AA.
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                                                                                       ; Search time 74.0755 Seconds (without alignments) 62.956 Million cell updates/sec
                                                                                                                                                                                                                                                                                              2002273
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                              2002273 segs, 358729299 residues
                                                                                           November 16, 2004, 14:09:48
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
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geneseqp2004s:*
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84
               Copyright
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                                                                                                                                                    Title:
Perfect score:
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Maximum DB
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                 Searched:
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                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abg60452 Selective	Abr56864 Aminopept	Abu20893 Protein e	Abg60448 Selective	Abr56860 Aminopept	Aaw13427 Breast tu	Aaw60290 Breast ca	Aaw93627 Breast tu	Aab17959 Integrin-	Aab17923 VEGF anta	Aab21702 Human bre	Aae06280 Human bre	Aau81104 Integrin-			_	Adj51706 CH1 delet	Abg66755 Human nov	Abg66701 Human nov	Adj69349 Human hea	Adl23265 Human MUC	Adj92337 Mouse hai	Gene	Aay65429 Human 5'	Himan
SUMMARIES	ID	ABG60452	ABR56864	ABU20893	ABG60448	ABR56860	AAW13427	AAW60290	AAW93627	AAB17959	AAB17923	AAB21702	AAE06280	AAU81104	ABB72956	ADJ73110	ADJ52745	ADJ51706	ABG66755	ABG66701	ADJ69349	ADL23265	ADJ92337	AAB39289	AAY65429	AAM95477
	DB	5	9	9	Ŋ	9	~	7	~	ო	m	ო	4	ß	ß	7	œ	œ	ഹ	ഹ	7	80	7	m	m	4
	Length	13	13	762	σ	σ	13	13	13	13	13	13	13	13	13	13	13	13	1364	1364	1594	5703	177	64	98	121
de	Query Match	100.0	100.0	60.7	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.8	58.3	57.1	57.1	57.1
	Score	84	84	51	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	49	48	48	48
	Result No.	1	7	М	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease.

Claim 22; Page 109; 317pp; English.

disease.

	Protei Drosop Drosop Wheat		Aacle207 Human MoL Add18192 Human mol Aac27065 Human Not Aay06816 Human Not
ABB96162 ABP69453 ABB898337 ABR41785 ABG60450 AABS662 AAB06124	ABU24443 ABB63025 ABB62331 AA021297	ABR43199 ABR43176 AAR80633 ABB69268	AAE18207 ADD18192 AAO27065 AAY06816
40000000	O 44 410 /	4 8 K 4 4	0 0 0 0
132	2165	414 478 573 1024	2469 2469 2471 2471
4444	0.00 0.00 0.00 0.00	4. 4. 4. 4. 8. 8. 8. 8. 8.	4. 4. 4. 4. œ. œ. œ. œ.
	י הטיטיטיטי		
4 4 4 4 4 4 4	4444	4 4 4 4 0 0 0 0	4444
26 20 30 33 33 33	8 8 8 8 6 4 8 9 6 6	3 8 4 4 4 3 9 11 0 0 9	2444 2644 2645

## ALIGNMENTS

Targeting peptide, cancer; arthritis, diabetes; inflammatory disease, atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; aradiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular Selective targeting peptide #127. 08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US027692. (first entry) (TEXA ) UNIV TEXAS SYSTEM. Pasqualini R; WPI; 2002-415731/44. WO200220769-A1 gene therapy. 14-MAR-2002. Synthetic. Arap W, 

Gaps

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Indels

Length 13;

100.0%; Score 84; DB 6; L 100.0%; Pred. No. 0.00011; iive 0; Mismatches 0;

13; Conservative

Local Similarity

Query Match Best Loc Matches

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for diagnosing the diseases citted above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60326-ABG60574 represent selective targeting peptides of the invention
inflammation or macular degeneration. Furthermore, the peptide is useful
                                                                                                                                                                                                                                                                                                                                                                                        peptide therapy, gene therapy, infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
                                                                                                                                                                                                                                                                                                                                                                          Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic;
                                                                                                                                                  Gaps
                                                                                                                                                ;
                                                                                                                     100.0%; Score 84; DB 5; Length 13; 100.0%; Pred. No. 0.00011;
                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                Aminopeptidase A (APA) binding peptide SEQ ID NO:60.
                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolonin MG;
                                                                                                                                                                                                                                                                    ABR56864 standard; peptide; 13 AA
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                                                                                                                                                                                                  1 CPKVCPRECESNC 13
                                                                                                                                                                         1 CPKVCPRECESNC 13
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                                                                                                                                                13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-371749/35.
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003022991-A2
                                                                                            Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-2003.
                                                                                                                                                                                                                                                                                              ABR56864;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                Matches
                                                                                                                                                                                                                                                     RESULT 2
8888888
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Bacteroides fragilis.

WO200277183-A2.

03-OCT-2002.

Protein encoded by Prokaryotic essential gene #6420.

(first entry)

19-JUN-2003

ABU20893;

ABU20893 standard; protein; 762 AA

RESULT 3 ABU20893

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid models acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated polypeptide whose expression is inhibited by the antisense controlled or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding controlleration or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene produce in the test compound that inhibits proliferation of an or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound sectivity; (11) a culture comprising strains in which the gene conjourned strains in which the compound that inhibits in which the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 48817; 1766pp; English.
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The present invention describes a method for treating obesity or a selective for adipose tissue; (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and dipose targeting peptides not anorectic and antilipaemic activities, and can be used in peptides have anorectic and antilipaemic activities, and can be used in peptides have morectic and antilipaemic activities, and can be used in peptides not gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immundeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABRS6806 to ABRS6827 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention

Sequence 13 AA;

New antisense nucleic acids, useful for identifying proteins or screening

for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

Wang L, Wall D,

WPI; 2003-029926/02

N-PSDB; ACA24763

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851, 06-MAR-2002; 2002US-0362699P.

(BLIT-) ELITRA PHARM INC.

21-MAR-2002; 2002WO-US009107. 21-MAR-2001; 2001US-00815242.

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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at from part of the printed secures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     5
                                                                                                                                                                                Length 762;
                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                              DB 6;
1e+02;
                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                  Score 51;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 ABG60448 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selective targeting peptide #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                60.7%;
60.0%;
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Best Local Similarity 60.0.
Best Society 60.0.
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                                                                                                                                              Sequence 762 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200220769-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy
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                                                                                                                                                                                                                                                                                            388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducting weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABRS6806 to ABRS6807 and ACC79106 to ACC7911 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                              Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a
                                                                  Gaps
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                                Score 50; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                Aminopeptidase A (APA) binding peptide SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 6; I
Pred. No. 1.7e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
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                                                                                                                                                                                                                             ABR56860 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arap W, Kolonin
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                                  59.5%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001; 2001WO-US027692
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88.9%;
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                     8; Conservative
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                                                                                                                                        CPRECESIC
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Best Local Similarity
Matches 8; Conserv
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003022991-A2
Sequence 9 AA;
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                                Query Match
Best Local S
Matches 8
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13

5 CPRECESNC

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Tumour homing molecules and their conjugates - useful for, e g. directing linked moiety to tumour containing angiogenic vasculature.
                                                                                                                                                                                                                                                                                                                                                                             by in vivo panning. The peptide homes to a breat carcinoma. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, collecting that the peptide that homes to the tumour, and determining that the peptide that homes peptide can be linked to a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug;
                                                                                                                                                                                                                                                                                                                                                                       peptide represents a tumour homing peptide, and is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prognosis, inflammation, regeneration, wounded tissue, targetting, macular degeneration, diabetic retinopathy, rheumatoid arthritis;
 Tumour homing peptide; in vivo panning; breast carcinoma; alpha-V-containing integrin binding motif; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%; Score 50; DB 2
53.8%; Pred. No. 3.8;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 6; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW93627 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast tumour homing peptide 1.
                                                                                                                                      97WO-US016086.
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98US-00139802
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                  (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                             WPI; 1998-207151/18.
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25-AUG-1998;
                                                                                                                                                                      10-SEP-1996;
                                               Unidentified
                                                                                                                                      10-SEP-1997;
                                                                           WO9810795-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                          19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW93627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This synthetic peptide is a claimed example of a breast tumour-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAW13412-52, AAW1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                    cancer; in vivo panning; screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%; Score 50; DB 2; Length 13; 53.8%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60290 standard; peptide; 13 AA.
                                                                           AAW13427 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 68; 75pp; English
                                                                                                                                                                                                  Breast tumour homing peptide; phage display; drug delivery.
                                                                                                                                                                                                                                                                                                                                         96WO-US014600.
                                                                                                                                                                    Breast tumour homing peptide.
                                                                                                                                                                                                                                                                                                                                                                     95US-00526708
                                                                                                                                                                                                                                                                                                                                                                                     95US-00526710
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : ||| |:||:|
1 CGRECPRLCQSSC 13
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-202359/18
 1 CPRECESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                          10-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1995;
                                                                                                                                                                                                                                                                             WO9710507-A1
                                                                                                                                      15-JAN-1998
                                                                                                                                                                                                                                                                                                            20-MAR-1997
                                                                                                                                                                                                                                               Synthetic.
                                                                                                        AAW13427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
AAW60290
ID AAW6
XX
AC AAW6
XX
DT 24-A
XX
DE Brea
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셤
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Gaps

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2; Length 13; Indels

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                                                                                                                                                                      vasculature, specifically of a tumour and which have anti-tumour, anti-
inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules
are identified by treating a purified NGR receptor with a test compound
and identifying compounds that bind specifically to the NGR receptor. The
peptides of the invention are inhibitors of angiogenesis and can be used
to produce conjugates for delivering agents to angiogenic vasculature,
particularly anticancer drugs or an imaging agent, for diagnosis or
prognosis. These conjugates may be directed to non-tumour angiogenic
ty asculature, e.g. that present in inflammatory, regenerating or wounded
tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
or rheumatoid arthritis. The peptides provide specific targeting to
thmours, especially their supporting vasculature, since the NGR receptor
is exposed to the circulation only in angiogenic vasculature. Precise
targeting should reduce the systemic toxicity of anticancer drugs in the
conjugates. Complete killing of all target cells may not be essential
since partial denudation of endothelium may result in an occlusive
thrombus, and endothelial cells are unlikely to become resistant to
anticancer agents nor to lose the targeting receptor. AAM93622-W93809 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                           that home to angiogenic vasculature used as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW93843-44 are examples of tumour homing peptides used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                            This invention describes novel peptides which home to angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.5%; Score 50; DB 2; Length 13; 53.8%; Pred. No. 3.8; 1:ve 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin-binding peptide sequence SEQ ID NO:1071.
                                                                                                                                   Example II; Page 67; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17959 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371P.
99US-00428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US025044
                                     Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : ||| |:|
1 CGRECPRLCOSSC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.8
Matches 7; Conservative
                                                                                           Identifying molecules
                                                                                                         for anticancer agents
             (BURN-) BURNHAM INST
                                                                 WPI; 1999-215158/18
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200024782-A2
                                      Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells from the present invention can be used for producing plarmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TFO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; cytotoxic; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 3; Length 13;
Pred. No. 3.8;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF antagonist peptide sequence SEQ ID NO:1027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
                                                                   Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                                                                                                                                                                                                                                                                              Claim 39; Page 589; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17923 standard; peptide; 13 AA.
                                                                   Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : ||| |:|| CGRECPRLCQSSC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.5
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                       WPI; 2000-350702/30
(AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000
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                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17923;
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Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer.
                                                                                                                                                                                                                                                                                                                         21-JAN-2000; 2000WO-US001602.
                                                                                                                                                                                                                                                                                                                                                          Ellerby HM, Bredesen DE,
                                                                                                                                                                    Local Similarity 53.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                               (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-499174/44.
                                                                                                                                                                                                                                                                                                   WO200042973-A2
                                                                                                                                                                                                                                                                                                                                    22-JAN-1999;
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                              27-JUL-2000.
                                                                                                                                                                                                                                       AAB21702;
                                                                                                                                                               Query Match
                                                                                                                                                                          Matches
                                                                                                                                                                                                                 RESULT 11
AAB21702
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The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is a homing peptide isolated in the present invention, which can be conjugated to an antimicrobial peptide to make the homing pro-apoptotic conjugates of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE06280 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 59.5%;
Local Similarity 53.8%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGRECPRICOSSC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE06280
       8888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each
independently selected from -(II)c-F1, -(II)c-P1-(I2)d-P2, -(IJ)c-P1-
(I2)d-P2-(I3)e-P3, or -(IJ)c-P1-(I2)d-P2-(I3)e-P3-(I4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; II, I2, I3, and I4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1

Cc, d, e, and f = are each independently 0 or 1, provided that at least 1

Cc of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Pab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent uncleotide and annon acid sequences used in the exemplification of the present invention
                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                         Claim 39; Page 557; 608pp; English.
                                                   WPI; 2000-350702/30.
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Gaps

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3; Indels

3; Mismatches

(first entry)

25-SEP-2001

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Gaps

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3; Indels

3; Mismatches

Score 50; DB 3; Length 13; Pred. No. 3.8;

59.5%;

AAE06280;

Score 50; DB 3; Length 13; Pred. No. 3.8;

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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic; human.
                                                                                                                                                                                                                                Arap W, Bredesen DE,
                                                     Human breast tumour homing peptide #1.
                                                                                                                                                                        16-JAN-2001; 2001WO-US001362.
                                                                                                                                                                                                                                 Ruoslahti EI, Pasqualini R,
                                                                                                                                                                                            21-JAN-2000; 2000US-00489582
                                                                                                                                                                                                              (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                    WPI; 2001-451901/48.
                                                                                                                                   WO200153342-A1.
                                                                                                                 sapiens.
                                                                                                                                                     26-JUL-2001
Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
                                                                                                                                                                                            Human breast tumour homing peptide #2.
                                                                                                                                    AAB21702 standard; peptide; 13 AA.
                                                                                                                                                                          22-MAR-2001 (first entry)
                                                                1 CPKVCPRECESNC 13
                                                                           1 CGRECPRLCOSSC 13
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is human breast tumour homing peptide. This sequence is useful in the homing of pro-apoptotic conjugates of the invention Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide. Example 5; Page 89; 176pp; English. Sequence 13 AA;

Pasqualini R, Ruoslahti EI;

99US-00235902

Example 5; Page 90; 118pp; English

Ellerby HM;

Gaps

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The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are compound on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (X'1) a-P'1-(X'2) b where; F'1 = Fc domain; X'1 and X'2 = (I'1) c-P'1-(I'1) c-P'1-(I'2) d-P'2-(I'3) e-P'3-(I'4) f-P'4; F'1-P'4 = same or different (I); L'1-L'4 = same or different linkers; a-f = 0 or 1, or vector containing the nucleic acid that encodes (Ia), provided at least one of a and b = 1, a nucleic acid that encodes (Ia), or vector, producing a pharmaceutically active compound (B) by covalently linking at least one Fc domain to at least one amino acid sequence of a selected randomized (I) and any of six laminin-related peptides (Ib). The compositions are used prophylactically and therapeutically in the same way as (I), e.g. to inhibit platelet automatodia arthritis) and many different forms of osteoporoass, also for diagnosis. Attaching the vehicle (eppecially forms) to (I) increases the half-life (free (I) are normally degraded contains the composition and containing the vehicle (eppecially contains).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quickly in vivo). The present sequence is an antagonist peptide of
                                                                                                                                                                                                                                                                                                                                                          IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory; immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper; echiestin; integrin; selectin; vinculin; platelet aggregation; angiogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has longer half-life than free peptide.
Score 50; DB 4; Length 13; Pred. No. 3.8;
                                       3; Indels
                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 19; 68pp; English.
                                                                                                                                                                                                                                                                                                                             Integrin-antagonist peptide #11.
                                                                                                                                                                                                           AAU81104 standard; peptide; 13
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59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0198919P.
03-MAY-2000; 2000US-0201394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001WO-US013069.
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                               | : ||| |:|:|
CGRECPRLCQSSC 13
                                                                        CPKVCPRECESNC 13
                                       7; Conservative
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200181377-A2
                                                                                                                                                                                                                                                                                     09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                  AAU81104;
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                                         Matches
                                                                                                                                                                        RESULT 13
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5.

В

59.5%; Score 50;

Sequence 13 AA;

Query Match

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The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antinflammatory, antitumour, immunosuppressive, cytostatic, antirhenmatic, antiathritic, antidiabetic, ophthalmological, antianaemic, anorectic, antinfertility, hemostatic, dermatological, cantianaemic, anorectic, antinfertility, hemostatic, dermatological and neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, infertility, and neurological degenerative diseases, (I), comprising compounds are useful for treating disorders characterised by low medic compounds are useful for treating disorders characterised by computed protein for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet tumour which result in thrombocytopaenia, splastic anaemia, metastatic tumour which result in thrombocytopaenia, splastic lupus erythematosus,
                         ö
                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TPO; tumour necrosis factor alpha inhibitor; interleukin 1 antagonist; IL antagonist; TTPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; TMP; cytostatic; antiinflammatory; antitumour; immunosuppressive; cytostatic; antiinflammatory; antitumour; antidiabetic; ophthalmological; antianaemic; antidiabetic; ophthalmological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; ellept disease; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                         ö
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gudas JM;
                         <u>ب</u>
  Pred. No. 3.8;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone TC,
                                                                                                                                                                                                                                                                                                                                                            Integrin binding peptide SEQ ID NO:1071.
                                                                                                                                                                                                                           ABB72956 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 47; 176pp; English
                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2001; 2001WO-US014310.
53.8%;
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                    1 CPKVCPRECESNC 13
                                                                                                             1 CGRECPRICOSSC 13
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130313/17.
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200183525-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                       ABB72956;
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                                                                                                                                                                              RESULT 14
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Gaps

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Indels

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portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an integrin binding peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel mammalian CDR mimetibodies, specific
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                       ö
                                                                                                              Score 50; DB 5; Length 13; Pred. No. 3.8; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scallon BJ, Ghrayeb J;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Integrin binding peptide sequence SeqID 564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 564; 97pp; English
                                                                                                                                                                                                                                                                                                                        ADJ73110 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-2003; 2003WO-US009139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2002; 2002US-0368791P.
                                                                                                              59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                        1 CPKVCPRECESNC 13
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1 CGRECPRLCQSSC 13
                                                                                                                              Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-804237/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003084477-A2.
                                                                             Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                             ADJ73110;
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                                                                                                                  Query Match
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59.5%; Score 50; DB 7; Length 13;

Sequence 13 AA;

Query Match

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3; Mismatches
                                                                                                    Search completed: November 16, 2004, 14:24:30 Job time : 78.0755 secs
  No.
  Pred.
53.8%;
                                        1 CPKVCPRECESNC 13
                                                        | : ||| |:|:|
CGRECPRLCOSSC 13
              Conservative
  Best Local Similarity
Matches 7; Conserv
                                         8
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 14:16:01; Search time 18.3962 Seconds

(without alignments)

46.865 Million cell updates/sec

10S-10-784-537-3

Perfect score: 84
Perfect score: 84
Sequence: 1 CPKVCPRECESNC 13
Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139
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se : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1071, Ap Sequence 6330, Ap Sequence 6784, A Sequence 105, Appli Sequence 1, Appli Sequence 16, Appli Sequence 16, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli 13710, A 6, Appli 7, Appli 8, Appli 6, Appli 7, Appli Description Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-139-802-2
US-09-659-786-2
US-08-659-786-2
US-09-428-082B-1071
US-09-428-082B-1071
US-09-210-76-42488
US-09-270-767-42488
US-08-5770-104-1
US-08-537-2104-1
US-08-185-432-16
US-08-185-432-16
US-08-185-432-16
US-08-181-19
US-08-181-19
US-08-489-0394-19
US-08-489-0394-19
US-09-481-250-7
US-09-481-250-6
US-08-454-255-7
US-08-454-255-7
US-08-454-255-8
US-08-431-500A-6
US-08-431-500A-6
US-08-431-500A-8 US-09-431-498-8 US-09-431-499-6 US-09-431-499-7 SUMMARIES DB Query Match Length 57. 1 Score Š. Result 

Sequence 8, Appli	Sequence 56916, A	Seguence 4416, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 104, App	Sequence 42636, A	Sequence 5543, Ap	Sequence 2852, Ap	Sequence 2986, Ap	Sequence 4019, Ap	Sequence 2, Appli	Sequence 7, Appli	Sequence 216, App	Sequence 216, App	Sequence 216, App
US-09-431-499-8	US-09-270-767-56916	US-09-513-999C-4416	US-08-454-295-3	US-09-431-500A-3	US-09-431-498-3	US-09-431-499-3	US-08-857-076-104	US-09-270-767-42636	US-09-134-000C-5543	US-09-710-279-2852	US-09-710-279-2986	US-09-134-001C-4019	US-08-737-715-2	US-09-457-040B-7	US-09-258-754-216	US-09-042-107-216	US-09-722-250D-216
4	4	4	m	m	4	4	ო -	4	4	4	4	m	7	m	m	e	4
58	77	163	368	368	368	368	370	429	478	480	480	490	1382	1382	13	13	13
52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	51.2	51.2	51.2
44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	43	43	43
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

```
Sequence 2, Application US/09139802

Sequence 2, Application US/09139802

Patent No. 6180084

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: NGR Receptor and Methods of Identifying Tumor Homing

ITILE OF INVENTION: Same

FILE REFERENCE: P-1303

CURRENT APPLICATION NUMBER: US/09/139,802

CURRENT PILING DATE: 1998-08-25

GURLER APPLICATION NUMBER: 08/926,914

EARLIER FILING DATE: 1997-09-10

EARLIER FILING DATE: 1996-09-10

NUMBER OF SEQ ID NOS: 226

SEQ ID NOS: 226

SEQ ID NOS: 226

SEQ ID NOS: 226
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; Sequence 2, Application US/09659786
; Sequence 2, Application US/09659786
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Rasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Same
; FILLE OF INVENTION: Same
; FILLE REFERENCE: P-LJ 3200
; FILLE REFERENCE: P-LJ 3200
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide
US-09-139-802-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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CGRECPRLCQSSC 13
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Matches 7; Conservative
US-09-139-802-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 13
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US-09-270-767-57784
                         RESULT 4
US-09-428-082B-1071
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US-09-621-976-6330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08926914
Patent No. 6576239
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: Peptide US-09-659-786-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 0.88;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                     59.5%; Score 50; DB 4; Length 13; ilarity 53.8%; Pred. No. 0.88; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR PILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-LJ 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.5%;
                                                                                                                                                                                       ORGANISM: Artificial Sequence
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1 CGRECPRLCQSSC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.5
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ČGREČPRLČQSSČ 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserve
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
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Sequence 1071, Application US/09428082B

Patent No. 6660843

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH

APPLICANT: CHEBTHAM, JANET C.

APPLICANT: CHEBTHAM, JANET C.

APPLICANT: CHEBTHAM, JANET C.

PREPARATION: THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-5.7

CURRENT APPLICATION NUMBER: US/09/428,082B

CURRENT FILING DATE: 1999-10-22

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SOFFWARE: Patentin version 3.1

SEQ ID NO 1071

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 4; Length 13;
Pred. No. 0.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6330
LENGTH: 98
TYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB Pred. No. 9.7; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-09-428-0828-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6330, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CPKVCPRECESNC 13
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Best Local Similarity 53.8
Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-09-621-976-6330
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Gaps

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Indels

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Mismatches

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2;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 CPS--PRDCESGC 224
                                                                  1 CPKVCPRECESNC 13
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86 CQTKCPEKCRNNC 98
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   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                              US-08-537-210A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-537-210A-1
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   Matches
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Sequence 42488, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburion:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICANTON NUMBER: US/09/270,767

CURRENT APPLICANTON NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 42488

LENGTH: 118
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Pred. No. 15;
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Pred. No. 8.2;
2; Mismatches 4; Indels
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                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-09-270-767-42488
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57784
LENGTH: 58
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53.8%;
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46.2%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-270-767-42488
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RESULT 9. 1200.

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Sequence 19, Application US/08083590A
Patent No. 5786158
Patent No. 5786158ch Proteins And TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STRRET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1; Length 247
Pred. No. 3.1e+02;
1; Mismatches 2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 31-JAN-1994
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
FELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
TELEPHONE: (212) 869-106
TELEPHONE: (212) 869-8864/9741
TELEPHONE: (212) 869-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COMPUTER: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSIFICATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1326-015
TELECOMMULCATION INFORMATION:
TELEFRAK: 212 8698864/9741
TELEFRAK: 212 8698864/9741
TELES: 6614 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.8%;
Best Local Similarity 61.5%;
Matches 8; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLEGULE TYPE: protein
US-08-185-432-16
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STRANDEDNESS: single
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Sequence 16, Application US/08185432

Patent No. 5750652

Patent No. 5750652

Patent No. 5750652

Patent No. 5750652

APPLICANT: Artavanis-Teakonas, Spyridon

APPLICANT: Busseau, Isabelle

APPLICANT: Matsuno, Kenji

APPLICANT: Matsuno, Kenji

TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND

TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                       TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Remnie & Edmonds
STREET: 1155 Pennie & Edmonds
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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OTHER INFORMATION: Highly conserved ankyrin repeat
OTHER INFORMATION: region of No. 6149902ch
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                                                                                                                                                                                                                             COUNTRY: USA
ZIF: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,210
FILING DATE: 29-5EP-1995
ATTORNEY/ACENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE DOCKET NUMBER: 7126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1015 amino acids
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MOLECULE TYPE: protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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APPLICANT: Artavanis-Tsakonas, Spyridon
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Patent No. 6083904

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS: 2

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                   Gaps
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                                                                           54.8%; Score 46; DB 1; Length 2471; 61.5%; Pred. No. 3.1e+02;
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61.5%; Pred. No. 3.1e+02;
usiamatches 2; Indels
                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
CUUTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: DATEMIN Release #1.0, Version #1.25
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
FLING DATE: PATEMIN 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
RILING DATE: 25-UUN-1993
ATTOMEY/AGENT INFORMATION:
                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7326-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Lealie
REGIGSTRATION UNUMBER: 18,072
REPRENCE/DOCKET NUMBER: 7326:
TELEPHONE: 212 790-9090
TELERX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                             1368 CPS--PRDCESGC 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
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                                                                                                                                                       1 CPKVCPRECESNC 13
                                                                                           Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity 61.5-
8; Conservative
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                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
TOPOLOGY: unknown
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STRANDEDNESS: siz
                         ; MOLECULE INF
US-08-083-590A-19
                                                                                                                                                                                                                                                       RESULT 13
US-08-532-384-19
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                                                                             Query Match
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US-08-899-232-1 ; Sequence 1, Application US/08899232 ; Patent No. 6436650 ; GENERAL INFORMATION:

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APPLICANT: Qi, Huilin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REPERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2471
                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: ATTACATION:
APPLICANT: ATTACATION:
APPLICANT: ATTACATION:
APPLICANT: ATTACATION:
APPLICANT: Q1, H.
APPLICANT: RAID
ACTIVATED OF INVENTION:
FILE OF INVENTION:
ACTIVATED OF INVENTION:
ACTIVATED OF INVENTION:
ACTIVATED OF INVENTION:
ACTIVATION NUMBER: US/09/121,457
CURRENT APPLICATION NUMBER: 08/899,232
EARLIER APPLICATION NUMBER: 08/899,232
EARLIER PILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 2471
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                                                                                                                                                                                                                                                                                 Length 2471;
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Sequence 1, Application US/09121457
Patent No. 6692919
GENERAL INFORMATION:
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Best Local Similarity 61.5
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                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conserva'
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November 16, 2004, 14:30:02 ; Search time 60.8302 Seconds (without alignments) 75.615 Million cell updates/sec
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(cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

(cgn2 6/ptodata/1/pubpaa/USO6 NEW_PUB.pep:*

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(cgn2 6/ptodata/1/pubpaa/USO8 NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 127, App	Sequence 48, Appl	Sequence 325327,	Seguence 48817, A	Sequence 123, App	Sequence 2, Appli	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	107	Sequence 1071, Ap	Sequence 1071, Ap	Sequence 1071, Ap
SUMMARIES	QI	US-10-363-204-127	US-10-411-910A-48	US-10-425-115-325327	US-10-282-122A-48817	US-10-363-204-123	US-09-765-086-2	US-09-840-277-32	US-10-264-374-2	US-10-375-992-2	US-10-609-217-1071	US-10-632-388-1071	US-10-651-723-1071	US-10-645-761-1071
	DB	16	17	11	15	16	o	o	14	14	15	15	15	15
	* Query Match Length DB	13	844	198	762	0	13	13	13	13	13	13	13	13
,	& Query Match	100.0	63.1	60.7	60.7	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5
	Score	84	53	51	51	20	20	20	20	20	20	20	20	20
	Result No.	п	7	m	4	2	9	7	60	σ	10	11	12	13

US-10-411-910A-48
; Sequence 48, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:

Sequence 1071, Ap Sequence 1071, Ap Sequence 2, Appli Sequence 2, Appli Sequence 1155, Ap	Sequence 2213, Ap Sequence 2213, Ap Sequence 125, App Sequence 105, App	Sequence 105, App Sequence 105, App Sequence 52651, A Sequence 52651, A		Sequence 2, Appli Sequence 2, Appli Sequence 12, Appl Sequence 145825, Sequence 58723, A Sequence 51212, A	
15 US-10-666-696-1071 15 US-10-653-048-1071 15 US-10-264-374-2 16 US-10-375-992-2 17 US-10-408-7658-1155 17 US-10-408-7658-1155	10 US-09-764-891-4135 15 US-10-264-237-2213 16 US-10-363-204-125 9 US-09-205-658-105	US-09-844-353A-105 0 US-09-963-693-105 	0 US-09-950-933A-52 1 US-10-425-115-304853 1 US-10-425-115-304851 15 US-10-419-026-1 16 US-10-322-281-726		17 US-10-425-115-293314 16 US-10-767-701-43605 17 US-10-425-115-314179 17 US-10-425-115-291729 17 US-10-425-115-314175 17 US-10-739-930-9529 17 US-10-425-115-208114
13 1 13 1 13 1 15 1 15 2			103 9 236 1 237 1 1015 1 2203 1	2469 2469 2471 181 145 1	1455 1252 1252 1252 1269 1369 146 146 149
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#### ALIGNMENTS

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Sequence 12. Application US/10363204

Publication No. US20040170955A1

GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents and Mouse Targeting Peptides Identified by Phage Display
FILE REPERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT PILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPKVCPRECESNC 13
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-363-204-127
                                                                                                                                                                                                                                                                                      LENGTH: 13
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Sequence 123, Application US/10363204
Sequence 123, Application US/10363204
Publication No. US20040170955A1
GENERAL INFORMATION:
APPLICANT: Board of E Regents, The University of Texas System
APPLICANT: Board of E Regents, The University of Texas System
TITLE OF INVERTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: 150/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOCTWARE: Patentin version 3.1
SEQ ID NO 123
LENGTH: 9
                                                                                                                       FILER KEFERRUCKE: BLITRA. US/10/282,122A
CURRENT PEDLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
                                        APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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88;
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OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacteroides fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 CGRVCPQEKQCESKC 402
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Best Local Similarity 60.03
Matches 9; Conservative
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Matches 8; Conservative
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           Forsyth, R.
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NAME/KEY: Peptide
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; Sequence 325327, Application US/10425115
; Publication No. US20040214272A1
; Garberal Information:
Garberal Application
Garberal Information:
Garberal Info
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APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes FILE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
UURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 29;
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US-10-425-115-325327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (1)..(198)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Travick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Sant
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53.8%;
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53.8%;
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Best Local Similarity 53.0
Ti Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                            SEQ ID NO 48
LENGTH: 844
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APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/10/264,374
CURRENT PILING DATE: 1098-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-05
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
PRIOR FILING DATE: 1996-09-10
SPRIOR FILING DAT
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TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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ADDRESSE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: Dubego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92122
COMPUTER READBELE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/375,992
FILING DATE: 27.Feb-2003
CLASSIFICATION: 435
S-10-264-374-2
Sequence 2, Application US/10264374
Publication No. US20030113320A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10375992
Publication No. US20030152578A1
GENERAL INFORMATION:
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Best Local Similarity 53.0-
7; Conservative
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APPLICANT: Wadih, Arap
APPLICANT: Wadih, Arap
APPLICANT: Wadih, Arap
APPLICANT: Bredseen, Dale E.
APPLICANT: Bredseen, Dale E.
APPLICANT: Bleaby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REFERENCE: P-Li 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT APPLICATION NUMBER: US 09/489,582
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 13
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APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LEB
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILLE REFERENCE: A-688A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT PELING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 135
NUMBER OF SEQ ID NOS: 135
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; OTHER INFORMATION: synthetic peptide
US-09-765-086-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09840277
Patent No. US20020168363A1
                                                          Sequence 2, Application US/09765086; Patent No. US20010046498A1
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1 CGRECPRLCOSSC 13
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1 CGRECPRLCQSSC 13
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Best Local Similarity 53.8
Matches 7; Conservative
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US-09-840-277-32
RESULT 6
US-09-765-086-2
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LENGTH: 13
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Query Match 59.5%; Score 50; DB Best Local Similarity 53.8%; Pred. No. 4.1; Matches 7; Conservative 3; Mismatches
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                                                                                                                                                                             OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-632-388-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
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CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1071, Application US/10645761 Publication No. US20040071712A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1071, Application US/10651723
Publication No. US20040057953A1
GENERAL INFORMATION:
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.6-
T; Conservative
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US-10-645-761-1071
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APPLICANT: LIU, CHUAN-PA
APPLICANT: LIU, CHUAN-PA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: GOONE, THOMAS CHARLES
TITLE OP INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE PALENT NOS: 1133
SOFTWARE PALENT NOS: 1133
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Publication No. US20040053845A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHECHAM, JANET C.
APPLICANT: BOOME, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                    Score 50; DB 14; Length 13;
Pred. No. 4.1;
3; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
                                                                                                                                    TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-375-992-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1071, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
                         TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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1 CGRECPRLCQSSC 13
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1 CGRECPRICQSSC 13
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Matches 7; Conservative
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US-10-632-388-1071
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LENGTH: 13
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APPLICANT: ILU, CHUAN-FA
APPLICANT: ILU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPRENCE: A-527
CURRENT APPLICATION NUMBER: US/10/651,723
CURRENT FILING DATE: 2003-08-29
FRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
FRIOR APPLICATION NUMBER: 60/105,371
SROFFWARE: PATENTING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: FIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHERTHAM, JANET C.
APPLICANT: BOONE; THOWAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
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DB 15; Length 13;
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Publication No. US20040077022A1

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH

APPLICANT: ELU, CHUAN-FA

APPLICANT: CHEETHAM, JANET C.

APPLICANT: GUDAS, JEAN MARIE

ITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527A

CURRENT APPLICATION NUMBER: US/10/666,696

CURRENT FILING DATE: 2003-09-19

FRIOR PILING DATE: 2000-05-03

FRIOR PILING DATE: 1999-10-22

PRIOR FILING DATE: 1998-10-22

PRIOR FILING DATE: 1998-10-23

FRIOR FILING DATE: 1998-10-23

WINGER OF SEQ ID NOS: 1157

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 1071

LENGTH: 133

TUDING DATE: 1998-10-23

LENGTH: 133
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; Sequence 1071, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FR
; APPLICANT: LIU, CHUAN-FR
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-S2;
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR PILING DATE: 1999-10-22
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Pred. No. 4.1;
3; Mismatches
                                                                                                   TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
JUSTIER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-666-696-1071
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                                                                                                                                                          Query Match 59.5%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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CGRECPRLCQSSC 13
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53.8%; Pred. No. 4.1;
tive 3; Mismatches 3
                                                                                                                                                                OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 16, 2004, 14:51:38 Job time: 69.8302 secs
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
LENGTH: 13
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                            1 CPKVCPRECESNC 13
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Best Local Similarity 53.8
Matches 7; Conservative
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November 16, 2004, 14:19:17; Search time 212.17 Seconds (without alignments) 67.889 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                6730630 seqs, 1107998698 residues
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Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                    1 CPKVCPRECESNC 13
                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                  US-10-784-537-3
84
                                                                                             Perfect score:
                                                                                                                      Scoring table:
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                                                                                                      Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scription	lequence 127, App lequence 60, Appl	equence 12/, App equence 3, Appli	equence 8, Appli	equence 5/04, Ap equence 5582, Ap	equence 5583, Ap	equence 5898, Ap equence 5795, Ap	equence 48, Appl	equence 48, Appi equence 92086. A	equence 5573, Ap	equence 325327, equence 92102. A	Sequence 5784, Ap	equence 48817, A equence 8497. Ap	equence 5770, Ap	equence 6, Appli	quence 123, App quence 56, Appl	equence 123, App	equence 2, Appil mence 2, Appli	quence 1027, Ap	quence 1071, Ap	equence 5, Appli equence 2, Appli	equence 2, Appli	equence 1071, Ap	equence 1071, Ap	equence 2, Appli equence 32. Appl	equence 32, Appl	equence 2, Appli	equence 2, Appii emience 1071 in	equence 1071, Ap	equence 1071, Ap	equence 1071, Ap	equence 10/1, Ap equence 10/1, Ap	equence 1206, Ap				System o Identified by Dhage Display	data official							
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ID	PCT-US01-27692A-127 PCT-US02-27836-60 US-10-263-204-127	US-10-363-204-12/ US-10-784-537-3	US-10-784-537-8	US-60-581-351-5/04 US-60-581-351-5582	US-60-581-351-5583	US-60-581-351-5898 US-60-581-351-5795	US-10-411-910A-48	US-10-763-712A-48 US-09-791-537-92086	US-60-581-351-5573	US-10-425-115-325327 US-09-791-537-92102	US-60-581-351-5784	US-10-282-122A-48817 US-09-540-209B-8497	US-60-581-351-5770	US-10-784-537-6	PCT-US02-27836-56	US-10-363-204-123	US-10-784-537-2 PCT-11500-01602-2	PCT-US99-25044-1027	PCT-US99-25044-1071	US-08-710-067-5	US-09-489-582-2	US-09-563-286B-1071	US-09-563-286C-1071	US-09-765-086-2 US-09-840-277-32	US-09-840-277B-32	US-10-264-374-2	US-10-3/5-992-2 TR-10-609-217-1071	US-10-632-388-1071	US-10-645-761-1071	US-10-651-723-1071	US-10-653-048-10/1 US-10-666-696-1071	US-60-143-992-1206	ALIGNMENTS		92A	versity of Texas	rargering reprind	9						construct
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Query Match	100.0	38	8	63.1	63.1	63.1	63.1	63.1	61.9	60.7	60.7	60.7	60.7	59.5	59.5	59.5	ט ע ע ע ע ע	59.5	59.5	5. 2. 3.	59.5	59.5	59.5	59.0 0.00	59.5	59.5	יי טיט יי	59.5	59.5		0 0 0 0	59.5		-127	APPIICA WATION:	pard of	JE: 005	NG DATE	o ID NO			rtifici	eptide	MATION:
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Gaps
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                                                                                                                                                                   Sequence 3, Application US/10784537

Sequence 3, Application US/10784537

GENERAL INFORMATION:
APPLICANT: PARCHALINI
APPLICANT: PASCUALINI
APPLICANT: PASCUALINI
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: PANIOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: PANIOPEPTIDASE
CURRENT APPLICATION NUMBER: US/10/784.537
CURRENT PILING DATE: 2004-02-23
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2000-09-08
SPINGR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 3
LEMENTH PARTICATION NUMBER: 60/231,266
PRIOR FILING DATE: 2000-09-08
SOFTWARE: PALCHIN VEY: 2.1
SEQ ID NO 3
LEMENTH PANIOR THE PALCHIN VEY: 2.1
LEMENTH PANIOR THE PALCHIN VEY: 2.1
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APPLICANT: PASQUALINI
APPLICANT: MARCHIO, SERENA
APPLICANT: LAHDENPANTA, JOHANNA
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
FILE REFERENCE: UTSC:872US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 84; DB 33; Length 13; 100.0%; Pred. No. 0.00018; tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/784,537
CURRENT FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: PCT/US02/27836
PRIOR PILING DATE: 2002-08-30
PRIOR PLILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR PELING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/765,101
PRIOR PLILING DATE: 2000-09-08
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/765,101
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 06/231,266
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN VET: 2.1
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GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 13; Conservative
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1 CPKVCPRECESNC 13
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TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: compositions and Adipose Tissues
FILE REPERENCE: 5774, P009PCT
CURRENT APPLICATION NUMBER: PCT/USO2/27836
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 144
SOGTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 13
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APPLICATION: Board of Regents, The University of Texas System

TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204

CURRENT FILING DATE: 2003-07

NUMBER OF SEQ ID NOS: 251

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                         Sequence 60, Application PC/TUS0227836
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               only)
Kolonin, Mikhail G. (applicant for the purpose of the United States of
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                      100.0%; Score 84; DB 1; Length 13; 100.0%; Pred. No. 0.00018; Live 0; Mismatches 0; Indels
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; OTHER INFORMATION: synthetic construct US-10-363-204-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Peptide PCT-US02-27836-60
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US-10-363-204-127
; Sequence 127, Application US/10363204
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 13; Conservative
                    Query Match
Best Local Similarity 100.
Matches 13; Conservative
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PCT-US02-27836-60
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APPLICANT:
APPLICANT:
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US-60-581-351-5704
US-60-581-351-5704
Sequence 5704, Application US/60581351
Sequence 5704, Application US/60581351
GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980-19
SOFTWARE: PatentIn version 3.2
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Sequence 5582, Application US/60581351

Sequence 5582, Application US/60581351

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

CURRENT APPLICATION NUMBER: US/60/581,351

PRIOR FILING DATE: 2003-06-19

NUMBER OF SEQ ID NOS: 13980

SOFTWARE: Patentin version 3.2

SEQ ID NO 5582

LENGTH: 464
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                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-784-537-8
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Pred. No. 50;
1; Mismatches 4; Indels
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US-60-581-351-5704
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; ORGANISM: Thermoanaerobacter tengcongensis
US-60-581-351-5582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.5%;
                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 92.3%;
Matches 12; Conservative
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87 CGRVCPQEEQCEKNC 101
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159 CGRVCPHTCESQC 171
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 500
SEQ ID NO 8
LENGTH: 12
                                              TYPE: PRT
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GENERAL INFORMATION:
Sequence 5583, Application US/60581351
GENERAL INFORMATION:
TATLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants FILE REFERENCE: 38-21(53372)8
FILE REFERENCE: 38-21(53372)8
CURRENT APPLICATION WUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION WHERE: US 60/479,962
NUMBER OF SEQ ID NOS: 13980
SOFWARE: Patentin Version 3.2
SEQ ID NOS: 5583
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REPERENCE: 38-21(53372)
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-19
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 649
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GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21 (53372) B
CURRENT PALLICATION NUMBER: US/60/581,351
CURRENT PAPLICATION NUMBER: US 60/479,962
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR PILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SEQ ID NO 5795
INVENTIOR OF SEQ ID NO 5795
TYPE: PRI
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Pred. No. 1.2e+02;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Thermoanaerobacter tengcongensis
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US-60-581-351-5898
; Sequence 5898, Application US/60581351
; GENERAL INFORMATION:
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; ORGANISM: Wolinella succinogenes
US-60-581-351-5898
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90 CGRVCPQETQCEKNC 104
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 60.vv
Best Local 9; Conservative
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JS-60-581-351-5583
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TYPE: PRT
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US-10-763-712A-48

i Sequence 48, Application US/10763712A

i GRUERAL INPORMATION:
    APPLICANT: Solazyme, Inc.
    APPLICANT: Dillon, Harrison F.
    TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
    TITLE OF INVENTION: Production
    TITLE OF INVENTION: Production
    TITLE OF INVENTION: Production
    TITLE OF INVENTION: Production
    FILE REFERENCE: H204201-CIP
    CURRENT APPLICATION UNMBER: US/10/763,712A
    CURRENT FILING DATE: 2004-01-21
    FRIOR FILING DATE: 2002-11-04
    FRIOR FILING DATE: 2003-04-12
    FRIOR PRICATION NUMBER: US 60/500,032
    FRIOR FILING DATE: 2003-09-03
    NUMBER OF SEQ ID NOS: 184
    SOFTWARE: Patentin version 3.2

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GENERAL INFORMATION:
PAPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
                                                           Score 53; DB 36; Length 672;
Pred. No. 1.2e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Desulfitobacterium hafniense US-10-411-910A-48
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; ORGANISM: Geobacter metallireducens
US-60-581-351-5795
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                               Query Match 63.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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177 CGRVCPHSCEAQC 189
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US-10-411-910A-48
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RESULT 13

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Sequence 92086, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 92086
LENGTH: 413
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Sequence 325327, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369327
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GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21 (53372) B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.9%; Score 52; DB 36; Length 413; 53.3%; Pred. No. 1.1e+02;
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Matches 8; Conservative
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Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps
) ORGANISM: Zea mays
; FRATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FRATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5976C.1.pep
US-10-425-115-325327
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76 CPKTCPNKCLAFC 88
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Search completed: November 16, 2004, 14:46:43 Job time : 213.17 secs

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RESULT 2
US-10-732-923-15015
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Sequence 15015, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 15841, A
Sequence 1464, App
Sequence 146, App
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146, App
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14210, A
20601, A
20601, A
14190, A
89, Appli
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                                                                                                                                           November 16, 2004, 14:24:42; Search time 14.0377 Seconds (without alignments) 40.083 Million cell updates/sec
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2: /cgn2 6/ptodata/1/paa/US06 NEW COMB.pep:*

3: /cgn2 6/ptodata/1/paa/US07 NEW COMB.pep:*

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8: /cgn2 6/ptodata/1/paa/US11 NEW COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-732-923-15015
US-10-874-049-1
US-10-874-049-1
US-10-80-120-366A-18045
PCT-US04-33017-4
US-10-95-128-4
US-10-95-952-146
US-10-95-952-146
US-10-95-952-146
US-10-95-952-146
US-10-95-952-14191
US-10-772-923-14191
US-10-732-923-14190
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US-10-732-923-14190
US-10-732-923-14190
US-10-732-923-14190
US-10-153-604B-89
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US-10-966-673-75
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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26 51.5 26.0 70 6 US-10-894-314A-256 Sequence 244, App 27 51.5 26.0 70 6 US-10-894-314A-256 Sequence 15.6, App 28 51.5 26.0 123 6 US-10-32-374-14 Sequence 16.7 App 29 51.5 26.0 145 6 US-10-320-36A-16237 Sequence 16.37, App 31 51.5 26.0 461 6 US-10-965-357-4 Sequence 16.37, App 21 51.5 26.0 461 6 US-10-965-357-6 Sequence 24, Appli 34 51.5 26.0 461 6 US-10-965-357-6 Sequence 26, Appli 34 51.5 26.0 461 6 US-10-965-357-8 Sequence 26, Appli 35 51.5 26.0 461 6 US-10-965-357-8 Sequence 27, Appli 36 51.5 26.0 461 6 US-10-967-851-8 Sequence 28, Appli 37 50.5 25.5 26 0 US-10-967-851-8 Sequence 1061, App 20.5 25.5 74 6 US-10-967-851-28 Sequence 1061, App 20.5 25.5 74 6 US-10-220-366A-15949 Sequence 15949, Appli 40 50.5 25.5 74 6 US-10-220-366A-15949 Sequence 15700, App 20.5 25.3 111 6 US-10-220-366A-15951 Sequence 15700, App 20.5 25.3 129 6 US-10-220-366A-15951 Sequence 15700, App 20.5 25.3 129 6 US-10-220-366A-15951 Sequence 15700, App 20.5 25.3 129 6 US-10-220-366A-15951 Sequence 15700, App 20.5 25.3 779 6 US-10-732-923-14192 Sequence 119, App 20.5 25.3 779 6 US-10-732-923-14192 Sequence 119, App 20.5 25.3 779 6 US-10-722-168 Sequence 119, App 20.5 25.3 779 6 US-10-732-923-14192 Sequence 119, App 20.5 25.3 779 6 US-10-732-923-14192 Sequence 119, App 20.5 25.3 779 6 US-10-702-119
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#### ALIGNMENTS

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RESULT 1

RESULT 1

RESULT 2

Sequence 59, Application US/10489071

GENERAL INFORMATION: COMPOSITIONS AND METHODS OF USE OF TRAGETING PEPTIDES AGAINST TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TRAGETING PEPTIDES AGAINST TITLE OF INVENTION: PLACETRY AND AD1POSE TISSUES

CURRENT APPLICATION NUMBER: US/10/489,071

TITLE OF INVENTION: PLACETRY AND AD1POSE TISSUES

CURRENT PELLOR DATE: 2004-03-08

FRIOR REPERENCE: 1002-08-00

NUMBER OF SEQ ID NOS: 144

SEQ OFTWARE PREPARED TO NOS: 1449

SEQ OFTWARE PREPARED TO NOS: 24149

SEQ OFTWARE PREPARED TO NOS: 24
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US-10-220-366A-18045
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APPLICANT: Shen, Annie
APPLICANT: Shen, Annie
APPLICANT: Seri, Annie
APPLICANT: Serila, Annie
APPLICANT: Sevilla, Blizabeth
APPLICANT: Aspelund, Amy
TITLE OF INVENTION: Subgroup B Adenovirus Vectors for Treating Disease
FILE REPERBUCE: ONYX 1053-ORD
CURRENT APPLICATION NUMBER: US/10/874,049
CURRENT FILING DATE: 2004-06-22
PRIOR PLING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                 APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Shen, Jerry Yuqiao
APPLICANT: Sevilla, Annie
APPLICANT: Sevilla, Elizabeth
APPLICANT: Sevilla, Elizabeth
APPLICANT: Sapelund, Any
TITLE OF INVENTION: Subgroup B Adenovirus Vectors for Treating Disease
FILE REFERENCE: ONYX 1053-ORD
CURRENT APPLICATION NUMBER: US/10/874,049
CURRENT FILING DATE: 2004-06-22
FRIOR APPLICATION NUMBER: US 60/488678
FRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.3
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Pred. No. 1.38+02;
2; Mismatches 14; Indels 1;
Score 67.5; DB 6; Length 895;
Pred. No. 3.1;
3; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.3%; Score 66; DB 6; Length 35823; Best Local Similarity 44.4%; Pred. No. 1.1e+02; Matches 12; Conservative 2; Mismatches 13; Indels
                                                                                                                         2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC 31
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                                                                                                                                                                                                                                                            Sequence 1, Application US/10874049 GENERAL INFORMATION:
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39.3%;
Query Match 34.1%;
Best Local Similarity 45.7%;
Matches 16; Conservative
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Best Local Similarity 39.39
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-874-049-2
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LENGTH: 35823
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Gaps
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GENERAL INFORMATION:
APPLICANT: University of Massachusetts
APPLICANT: LAMBRIGHT, David G.
APPLICANT: CZECH, Michael P.
APPLICANT: CZECH, Michael P.
APPLICANT: CRONIN, Thomas
TITLE OF INVENTION: PLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
TITLE OF INVENTION: PLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
CURRENT APPLICATION NUMBER: PCT/US04/33017
CURRENT FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 18045, Application US/10220366A

Sequence 18045, Application US/10220366A

GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A

CURRENT PILING DATE: 2002-0828

PRIOR PILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-05-18

PRIOR PILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27802

SOFTWARE: CUENCEM

SEQ ID NO 18045
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i OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-18045
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; Sequence 4, Application US/10962128
; GENERAL INFORMATION:
APPLICANT: LAMBRIGHT, David G.
; APPLICANT: CZECH, Michael P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.83
Matches 11; Conservative
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ORGANISM: Homo sapiens
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Sequence 146, Application US/10955952 GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                   10; Conservative
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              SEO ID NO 14903
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-10-955-952-146
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Matches 10; Conserv
SOFTWARE: Custom
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APPLICANT:
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              TITLE OF INVENTION: VARIANT POLYPEPTIDES CONTAINING
TITLE OF INVENTION: PLEKSTRIN HOMOLOGY DOMAINS AND USES THEREFOR
FILE REPERENCE: UMY-086
CURRENT APPLICATION NUMBER: US/10/962,128
CURRENT FILING DATE: 2004-10-07
PRIOR PILLING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 2127-2042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 2001-02-3
NUMBER: OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 15841
LENGTH: 123
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OTHER INFORMATION: Xaa = any amino acid or nothing
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45.8%; Pred. No. 70;
tive 2; Mismatches
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US-10-220-366A-15841
Sequence 15841, Application US/10220366A
GENERAL INFORMATION:
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Best Local Similarity 45.8'
Matches 11; Conservative
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Best Local Similarity 29.09
Matches 9; Conservative
CRONIN, Thomas
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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LENGTH: 1602
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APPLICANT:
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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TILLE OF INVENTION: ACIDS ENCODING THE SAME

FILE OF INVENTION NUMBER: US/10/121,058

PRIOR PLINGO DATE: 2002-04-12

PRIOR PELING DATE: 1997-06-18

PRIOR PILING DATE: 1997-06-18

PRIOR PLING DATE: 1997-06-18

PRIOR PELING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PLING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-19

PRIOR PLING DATE: 1997-09-19
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(119)
; OTHER INFORMATION: Kaa = any amino acid or nothing US-10-220-366A-14903
                                                                                                                                                                                                                                                 27.8%; Score 55; DB 37.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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Wood, William
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 13; Conserva
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R16426
CURRENT APPLICATION NUMBER: U5/10/157,779
CURRENT PILING DATE: 2002-05-29
PRIOR PELING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-09-19
                                                        Gaps
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           DB 6; Length 945;
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                                                        9; Indels
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; Pred. No. 70;
1; Mismatches
         Score 54.5; DI
Pred. No. 70;
1; Mismatches
                                                                                                                                                                                                                                                             Sequence 146, Application US/10157779 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-09-19
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           27.5%;
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Watanabe, Colin K
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
Query Match
Best Local Similarity 40.67
Matches 13, Conservative
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Best Local Similarity 40.6
Matches 13, Conservative
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; ORGANISM: Homo Sapien
US-10-157-779-146
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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C33

CURRENT APPLICATION NUMBER: US/10/964,241

CURRENT FILING DATE: 2004-10-12

PRIOR APPLICATION NUMBER: PRIORT APPLICATION NUMBER: US/10/123,236

PRIOR APPLICATION NUMBER: 60/049911

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-16

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059113

PRIOR PLING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR APPLICATION NUMBER: 60/059117

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059263

PRIOR APPLICATION NUMBER: 60/059363

PRIOR PLING DATE: 1997-09-19

PRIOR PLING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 791CIP4
CURRENT APPLICATION NUMBER: US/10/972,024
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: PCT/US01/08655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 CTTİCPVDGAWTEWSKWSACSİECAHWRSREC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CESICGADG-----ACWIWCADGCSRSC 31
Sequence 146, Application US/10964241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 292, Application US/10972024 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe, Colin K
                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                            Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherwood, Steven
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TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 14191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52785) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 14210
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.5%; Score 54.5; DB 6; Length 994; Best Local Similarity 32.5%; Pred. No. 73; Matches 13; Conservative 4; Mismatches 12; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 27.5%; Score 54.5; DB 6; Best Local Similarity 40.6%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 CTTICPVDGAWTEWSKWSACSTECAHWRSREC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 CESICGADG-----ACWIWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR PELING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-34
PRIOR PILING DATE: 2000-10-01
PRIOR PILING DATE: 2001-02-01
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-03-22
NUMBER: 09/816,828
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-732-923-14210
; Sequence 14210, Application US/10732923
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14191, Application US/10732923
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-14191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT;
CRGANISM: Homo sapiens
US-10-972-024-292
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; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-732-923-14210
US-10-732-923-14210

Query Match
Best Local Similarity 30.6%; Pred. No. 79;
Matches 11; Conservative 3; Mismatches 15; Indels 7; Gaps 1;

Qy 1 CYNLC-----IRECESICGADGACWWCADGCSR 29

Qy 1 CYNLC------IRECESICGADGACWWCADGCSR 29

Db 698 CGELCNKLLSCKTHFCEKLCHPDGECESSCKKECGK 733

Search completed: November 16, 2004, 14:47:12
Job time: 15.0377 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03 ; Search time 35.0943 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-1 198 1 CYNLCIRECESICGADGACWTWCADGCSRSC 31 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	hypothetical prote	_	귽	•	depressant insect	a,	hypothetical prote	_	_	_	9	hypothetical prote	_	hypothetical prote	岩	hypothetical prote	_	끍	hypothetical prote	protein C24B5.5 [i	ultra-high-sulfur	ultra-high-sulfur	lectin-B - Virgini	probable proteinas		CT105 hypothetical	hypothetical prote	cal	2
	ОП	T30136	T23271	B34123	S52093	A61616	T23681	T23682	T22099	T22100	T22102	A21761	T20561	T23680	T27686	T52415	T01503	T32497	A40472	T20283	G89152	B38346	A38346	JC5559	861553	S23061	C86541	D72082	T25169	EGRT
	DB	0	~	~	7	~	7	~	~	7	~	~	7	7	7	7	N	7	7	~	~	~	~	~	~	~	~	~	~	-
	Length	654	662	61	3133	85	1513	294	163	163	164	124	728	372	314	856	868	2150	82	103	328	223	230	295	74	105	258	258	330	1133
م م م	Match	36.4	35.1	33.8	33.1	32.3	32.3	32.1	31.6	31.6	31.6	31.1	30.6	30.3	30.1	30.1	30.1	30.1	29.8	29.8	29.8				ę.	e.	æ	28.8	28.8	28.8
	Score	72	69.5	67	65.5	64	64	•	62.5	62.5	62.5	ä	60.5	9	٠	•	59.5	•	59	59	29	ä	58.5	ä	٠	7.	57	57	57	57
Pegult	No.		7	٣	4	'n	9	7	Φ	60	10	11	12	13	14		16	17	18	19	20	21	22	23	24	25	56	27	28	53

35.1%; Score 69.5; DB 2; Length 662; 44.4%; Pred. No. 2;

Query Match Best Local Similarity

alpha tectorin - c	depressant insect-	depressant insect-	regulator protein	Balbiani ring 3 pr	zonadhesin - pig	von Willebrand fac	depressant insect-	hypothetical prote	hypothetical prote	excitatory insect	neurotoxin I' prec	probable expressio	protein R09B5.5 (i	hypothetical prote	insulin receptor -
T30243	A59352	B59352	JE0394	S08167	T34022	VWHU	C59352	T35190	T23802	A59006	NTSRIZ	T36770	A88949	T29880	T30346
7	~	N	~	N	~	н	~	N	N	~	н	N	N	N	~
2120	61	61	310	1700	2476	2813	61	534	358	61	83	272	388	572	1390
28.8	28.5	28.5	28.5	28.5	28.5	28.5	28.3	28.3	28.0	27.8	27.8	27.8	27.8	27.8	27.8
57	56.5	56.5	56.5	56.5	56.5	56.5	26	26	55.5	55	25	55	25	55	22
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 T30136 hypotein clack of the control of th	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-654 cDUZ> A;Residues: 1-654 cDUZ> A;Residues: 1-654 cDUZ> A;Cross-references: UNIPROT:Q17982; EMBL:U53141; PIDN:AAA96110.1; GSPDB:GN00023; CESP:C14 A;Experimental source: strain Bristol N2; clone C14C11 C;Genetics: A;Gene: CESP:C14C11.8 A;Map position: 5 A;Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3 A;Introns: 50/3; 98/3; 155/3; Pred. No. 1.1; Best Local Similarity 32.3%; Pred. No. 1.1; Best Local Similarity 32.3%; Pred. No. 1.1; Matches 10; Conservative 7; Mismatches 14; Indels 0; Gaps 0;	Oy 1 CYNLCIRECESICGADGACWIWCADGCSRSC 31	A; Reference number: Z19719 A; Accession: T2371 A; Accession: T2371 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-662 <wil> A; Residues: 1-662 <wil> A; Residues: 1-662 <wil> A; Residues: clone K03D10 A; Experimental source: clone K03D10 C; Genetics: A; Gene: CESP: K03D10.1 A; Map position: 1 A; Map position: 1 A; Map position: 1 A; TATA POSITION: 1 A; TATA POSITION: 23/3: 78/3: 597/3</wil></wil></wil>
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33.1%; Score 65.5; I
46.7%; Pred. No. 16;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.3%;
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                         Local Similarity 46.7
hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A61616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 9; Conserv
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A;Gene: CESP:M02G9.1
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R; Matthews, L.
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  Query Match
Best Local Si
Matches 14;
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C;Species: Bombyx mori (silkworm)
C;Species: Bombyx mori (silkworm)
C;Accession: S52093; S70920
R;Kotani, E.; Yamakawa, M.; Iwamoto, S.; Tashiro, M.; Mori, H.; Sumida, M.; Matsubara, F
Biochim. Biophys. Acta 1260, 245-258, 1995
A;Title: Cloning and expression of the gene of hemocytin, an insect humoral lectin which
A;Reference number: S52093; MUID:95178544; PMID:7873598
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-61 <ZLO1.
A;Cross-treferences: UNIPROT:P19855
R;Kopeyan, C.; Mansuelle, P.; Sampieri, F.; Brando, T.; Bahraoui, E.M.; Rochat, H.; Gran
PEBS Lett. 261, 423-426, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-61 <KOP>
R;Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler, Bicchemistry 30, 4814-4821, 1991
A;Title: Functional duality and structural uniqueness of depressant insect-selective neu A;Reference number: A38526; MUID:91230120; PMID:2029523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Title: Primary structure of scorpion anti-insect toxins isolated from the venom of Reference number: S08267; MUID:90184494; PMID:2311768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
     ä
                                                                                                                                                                                                                   depressant insect toxin LqqIT2 - scorpion (Leiurus quinquestriatus)
C;Species: Leiurus quinquestriatus quinquestriatus
C;Date: 06-Jul-1990 #sequence revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: B34123; S08268; B38526
Toxicon 18:, Fowler, E.; Eitan, M.; Moyer, M.; Adams, M.E.
Toxicon 28, 170, 1990
A;Title: On the chemistry and action of the depressant insect toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
       Gaps
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: neurotoxin; venom
F;10-60,14-35,21-42,25-44/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1566,'S',1568-3133 <MOR>
A;Cross-references: EMEL:D29738; NID:9474967; PID:9664884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 2
Pred. No. 0.73;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: P98092; EMBL: D29738
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, April 1994 A;Reference number: S70920 A;Accession: S70920
                                                                                                79 ECSALCOMDGECPETOXCCSSGCSROC 105
                                                ECESICGADGAC -- - WTWCADGCSRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: hemolectin/hemocytin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein
Residues: 1-61 <ZLO2>
Cross-references: CAS:130300-67-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CIRECESICGADGACWTW 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%;
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Best Local Similarity 55.65
Matches 10; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A34123
A;Accession: B34123
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A; Residues: 1-3133 <KOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nemocytin - silkworm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S08268
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     12;
  Matches
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depressant insect toxin LghIT2 precursor - scorpion (Leiurus guinquestriatus)
C;Species: Leiurus guinquestriatus hebraeus
C;Date: 21-Jul-1995 #sequence revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: A61616; A34123; Ā38526
C;Accession: A61616; A34123; Ā38526
Insect Biochem. Mol. Biol. 22, 199-203, 1992
A;Title: Molecular analysis of cDNA and the transcript encoding the depressant insect sel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 22-82 -22.02.01.
R;Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler, I
Biochemistry 30, 4814-4821, 1991
A;Title: Punctional duality and structural uniqueness of depressant insect-selective neum
A;Reference number: A38526; MUID:91230120; PMID:2029523
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A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Residues: UNIPROT:O17970; EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M05
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A; Residues: 22-82 < ZLD2>
A; Cross-references: CAS:13300-64-0
C; Superfamily: scorpion neurotoxin
C; Superfamily: scorpion neurotoxin
C; Superfamily: scorpion neurotoxin
F; 1-1/Domain: signal sequence #status predicted < SIG>
F; 12-21/Domain: propeptide #status predicted < RGS>
F; 22-82/Product: depressant insect toxin #status experimental < MAT>
F; 31-81, 35-56, 42-63, 46-65/Disulfide bonds: #status predicted
F; 82/Modified site: amidated carboxyl end (Gly) (amide in mature form from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                        Gaps
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A;Nalecule type: mRNA
A;Residues: 1-85 <ZIL>
A;Cross-references: UNIPROT:026292
B;Zlotkin, E.; Fowler, E.; Eltan, M.; Moyer, M.; Adams, M.E.
Toxicon 28, 170, 1990
A;Title: On the chemistry and action of the depressant insect toxins.
A;Reserence number: A34123
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                                                                     3;
DB 2; Length 3133;
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Pred. No. 1.9;
4; Mismatches 5; Indels
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hypothetical protein F42F12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T22100
C;Accession: T22100
S;Alloyd, C.
Submitted to the EMBL Data Library, November 1995
A;Reference number: Z19514
A;Accession: T22100
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule rype: DNA
A;Residues: 1-163 - WIA
A;Residues: 1-164 - WIA
A;Residues: 1-165 - WIA
A;Residues: 1-165 - WI
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submitted to the EMBL Data Library, November 1995
A;Accession: T22102
A;Accession: T22102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-164 <WIL>
A;Cross-references: UNIPROT: Q20345; EMBL: Z68116; PIDN: CAA92174.1; GSPDB: GN00028; CESP: P4;
A;Experimental source: clone F42F12
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22102
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C;Superfamily: Caenorhabditis elegans hypothetical protein F42F12.1
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31.6%; Score 62.5; DB 2; Length 163;
Best Local Similarity 41.9%; Pred. No. 4.4;
Matches 13; Conservative 4; Mismatches 9; Indels
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31.6%; Score 62.5; DB 2; Length 164;
Best Local Similarity 41.9%; Pred. No. 4.4;
Matches 13; Conservative 4; Mismatches 9; Indels
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A,Molecule type: DNA
A,Residues: 1-124 <IAT>
C,Superfamily: chorion class A protein pc292
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Cacession: T23682
R;Matchlews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219781
A;Reference number: 219781
A;Reference number: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-294 <MIL>A;Residues: 1-294 <MIL>A;Residues: 1-294 <MIL>A;Residues: Clone M02G9
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A;Cross-references: UNIPROT:Q20342; EMBL:Z68116; PIDN:CAA92171.1; GSPDB:GN00028; CESP:P4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22099
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                       A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.1%; Score 63.5; DB 2; Length 294; Best Local Similarity 35.5%; Pred. No. 5.2; Matches 11; Conservative 5; Mismatches 14; Indels 3
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                                                                                                                              Query Match 32.3%; Score 64; DB 2; Length 1513; Best Local Similarity 35.5%; Pred. No. 14; Matches 11; Conservative 2; Mismatches 18; Indels
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A,Molecule type: DNA
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submitted to the EMBL Data Library, November 1995
A;Reference number: 219514
A;Accession: T22099
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A;Introns: 20/3; 76/2; 182/3; 223/3
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A;Gene: CESP:F42F12.7
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T22100
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A,Map position: 2
A,Introns: 30/3; 296/2
C,Superfamily: gliadin
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A;Gene: CESP:ZK1067.7
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A;Molecule type: DNA
A;Residues: 1-37. «MIL»
A;Cross-references: UNIPROT:017969; EMBL:Z81573; PIDN:CAB04624.1; GSPDB:GN00020; CESP:MC
A;Experimental source: clone M0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-728 <WIL>
A;Cross-references: UNIPROT:Q19182; EMBL:Z68314; PIDN:CAA92662.1; GSPDB:GN00020; CESP:FG
A;Experimental source: clone F07H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23680
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F07H5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Query Match 31.1%; Score 61.5; DB 2; Length 124; Best Local Similarity 31.0%; Pred. No. 4.7; Matches 13; Conservative 2; Mismatches 16; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 2; Length 372;
Pred. No. 15;
4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                1 CYNLCIRECESICGADGACWTWCAD------GCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2
A;Introns: 17/3; 72/3; 181/3; 232/2; 258/3; 294/3; 336/1
C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 | : | : | : | : | 323 | 334 | 334 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 335 | 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1996 A;Reference number: 219781 A;Accession: T23680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Risteward, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 60.5; DE ilarity 30.6%; Pred. No. 20; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 2
A;Introns: 32/3; 81/3; 489/3; 591/3; 633/3
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Best Local Similarity 31.4%;
Matches 11; Conservative 4
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les 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:F07H5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: T20561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
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Matches
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T27686 hypothetical protein ZK1067.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

RESULT 14

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A;Residues: 1-314 <WIL>
A;Cross-references: UNIPROT:Q23390; EMBL:Z70038; PIDN:CAA93886.1; GSPDB:GN00020; CESP:ZK1
A;Experimental source: clone ZK1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polycomb protein EZA1 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C; Accession: T55415
R; Bilodeau, P.; Luo, M.; Dennis, E.S.; Peacock, W.J.; Chaudhury, A.M. submitted to the BMBL Data Library, October 1998
A; Reference number: Z26069
A; Accession: T52415
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T27686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.1%; Score 59.5; DB 2; Length 856; Best Local Similarity 46.4%; Pred. No. 29; Matches 13; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.1%; Score 59.5; DB 2; 29.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-856 <BIL>
                                                                                                              A;Reference number: Z20404
A;Accession: T27686
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CIPVCLAQCQSSC-QTSQCIQQCQPACNQQC 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Thomas, K.
submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CESICGADGACWT--WCAD---GCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 16, 2004, 14:30:50 Job time: 37.0943 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.0%
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prion.
SEQUENCE
                                                                                                                                                                                                                                                                               Wilson R.;
RESULT 1
Q17982
062299 caenorhabdi
Cabwa94 caenorhabdi
Cae48500 caenorhab
Cae48500 caenorhab
O88404 cae mays (m
08140 coryca sativ
091106 coryca sativ
P19855 leiurus qui
P98092 bombyx mori
P92716 arabidopsis
O8brce mus musculu
O7unp4 rhodopirell
66094 drosophila
Aar82794 drosophila
099qru drosophila
099qru drosophila
099qru drosophila
096890 drosophila
Q8690 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P55903 buthus occi
P55904 buthus occi
Q26292 leiurus qui
O17970 caenorhabdi
Q8ilm9 plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9xus0 caenorhabdi
Q23947 drosophila
Q23948 drosophila
Q20342 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q868z9 drosophila
P80962 buthacus ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmodium
caenorhabdi
                                                                                                                                                                                                                                                                                                                          Q17982 caenorhabdi
                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    ; ; Search time 184.83 Seconds (without alignments) 96.503 Million cell updates/sec
                                                                                                                                                      1825181
        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                       1825181 segs, 575374646 residues
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Q869A0
Q7KRX2
AAF56795
Q868Z9
SIX2_BUTAR
SIX4_BUTOC
SIX5_BUTOC
SIX5_BUTOC
O17970
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HMCT_BOMMO
LCR1_ARATH
Q8BRC8
                                                     November 16, 2004, 14:14:16
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q8WS94
CAB04551
CAE48500
EZ3 MAIZE
Q84ŪI6
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Q6NP04
AAR82794
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023947
023948
020342
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
                                                                                  US-10-784-537-1
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2772
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                                      OM protein
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Maximum DB
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                                                                                                                                       Searched:
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Q20345 caenorhabdi
Q814j0 caenorhabdi
Q814j1 caenorhabdi
Q814j2 caenorhabdi
Q81043 caenorhabdi
Q81042 mus musculu
Q811g8 mus musculu
Q71ng6 mus musculu
Q71ng6 mus musculu
Q71c30 giardia lam
Q61534 mus musculu
Q81c8 mus musculu
Q81c8 mus musculu
Q81c8 mus musculu
Q81c8 mus musculu
Q81c8 mus musculu
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                       Q17982 PRELIMINARY, PRT; 572 AA.
Q17982,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Prion-like (Q/n-rich)-domain-bearing protein protein 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 2;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                 WFD3_HUMAN
Q8R1G8
Q8R1H9
Q7TNG6
Q7R630
                                                                                                                                                                                              Q61834
AAH69956
   Q20345
Q814J0
Q814J1
Q8WQG6
Q20343
                                                                                                                                                                                                                                   QBROKB
QBKOP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (JUN-2004) to the EMBI
EMBL; U53141; AAA96110.3; -.
PIR; T30136; T30136.
HSSP; P56679; 1PBI.
WormPep; C14C11.8; CE27684.
InterPro; IPR003341; DUF139.
InterPro; IPR006209; EGF_like.
Pfam; PF02363; C tripleX; 15.
PROSITE; PS01186; EGF_2; 1.
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657
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Caenorhabditis elegans.
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STRAIN=Bristol N2;
Du Z., Gattung S.;
Submitted (APR-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (NOV-2002) t
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Gaps
          Name=kal-1;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                         Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF342986; AAL73338.1; -
InterPro; IPR003951; FN III.
InterPro; IPR008957; FN III.
Pfam; PR00041; fn3; 3.
Pfam; PR00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 69.5; DB 2; Length 700; 44.4%; Pred. No. 3.7; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-1004 (TremBLrel. 27, Last annotation update)
C. elegans KAL-1 protein (Corresponding sequence K03D10.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White S.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z81561; CAB04551.2; -.
EMBL; Z92828; CAB04551.2; JOINED.
SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                                                                                                                                                            78584 MW; 2975913064E981E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 AA
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                                                                                                                                                                                                                                                                                                                                                                              8 ECESICGADGAC---WIWCADGCSRSC 31
                                                                                                                                                                                                                      PRINTS; PRO0003; 4DISULPHCORE.
SWART; SM00060; FN3; 3.
SMART; SM0017; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
PROSITE; PS50853; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 44.44 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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es 12; Conserva
                                                                                                                                                                                                                                                                                             700 AA;
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                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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CAB04551;
                                                                                                                                                                                                                                                                                             SEQUENCE
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CAE48500
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 700;
                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
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 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00317; 4 DISULPIDE_CORE; 1.
PROSITE; PS50853; FN3; 2.
Hypothetical_protein.
SEQUENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
10-CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein K03D10.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBlrel. 20, Created)
(TremBlrel. 20, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.1%; Score 69.5; DB 2; Best Local Similarity 44.4%; Pred. No. 3.7; Matches 12; Conservative 3; Mismatches 9;
                                           452 CVQACQPQCQQTCGSNVQCVSACQNSCQQSC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 AA
                       1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
7; Mismatches
                                                                                                                            700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 ECSALCOMDGECPETOKCCSSGCSROC 143
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                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; K03D10.1; CE18005.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR008197; WAP.
                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 281561; CAB04551.2; -...
EMBL; 292828; CAB04551.2; JOINED.
EMBL; 2918161; CAE48500.1; JOINED.
EMBL; 292828; CAE48500.1; -...
PIR; T23271; T23271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00060; FN3; 3.
SMART; SM00217; WAP; 1.
 10; Conservative
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                                                                                                                           PRELIMINARY;
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Pfam; PF00095; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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01-MAR-2002 (
01-OCT-2003 (
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Q8WS94;
                                                                                                                                        062299;
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Q8WS94
ID Q8WS
AC Q8WS
DT 01-M
DT 01-M
Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A POLYCOMB group gene of rice (Oryza sativa L. subspecies indica), OsiEZ1, codes for a nuclear-localized protein expressed preferentially in young seedlings and during reproductive development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22890056; PubMed-14527713;
Thakur J.K., Malik M., Bhatt V., Reddy M.K., Sopory S.K., Tyagi A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.1%; Score 67.5; DB 1; Length 895; 42.9%; Pred. No. 8.1; ive 4; Mismatches 9; Indels "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 78 Poly-Ala.
895 AA; 100392 MW; 2659DCF992A08919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99775 MW; BB618FCD0E414FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             647 YNPCV--CQQMCGKDCPCVENGTCCEKYCGCSKSC 679
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SMART; SM00717; SANT; 1.
SMART; SM00317; SET; 1.
PROSITE; PS50210; SET; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       895 AA
                                                                                                                                                                                                                                                                                  InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR001214; SET.
Ffam; PP00856; SET; 1.
SMART; SM00717; SANT; 1.
SMART; SM00317; SET; 1.
PROSITE; PS50090; WYB 3; FALSE_NEG.
PROSITE; PS50280; SET 1.
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Cys-rich.
SIMILARITY: Contains 1 SET domain.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR001214; SET.
InterPro; IPR008197; WAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANT.
                                                                                                                                                                                                                                     EMBL; AF443598; AAM13422.1; -.
MaizeDB; 754846; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhancer of zeste protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003
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Q84UI6
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1. FUNCTION: Polycomb group (PGG) protein. PGG proteins act by forming multiprotein complexes, which are required to maintain the transcriptionally repressive state of homeotic genes throughout but to maintain it during later stages of development. They probably act via the methylation of histones, rendering chromatin probably act via the methylation of histones, rendering chromatin heritatibly changed in its expressibility. Its sequence suggests that it may participate in a potential methyltransferase activity of PCG complexes (By similarity).

1. SUBCELLUIAR LOCATION: Nuclear (Probable).

2. IISSUE SPECIFICITY: Widely expressed.

2. SIMILARITY: Belongs to the EZ family.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.1%; Score 69.5; DB 2; Length 700; 44.4%; Pred. No. 3.7;
                                                                       -MAR-2004 (TrEMBLrel. 27, Last sequence update)
-MAR-2004 (TrEMBLrel. 27, Last annotation update)
elegans KAL-1 protein (Corresponding sequence K03D10.1).
                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Seed;
MEDLINE=21948211; PubMed=11950982; DOI=10.1104/pp.010742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White S.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUDDILLOCA (AL. 1875).
EMBL; 291561; CAE48500.1; -.
EMBL; 281561; CAE48500.1; JOINED.
CROTTENCE 700 AA; 78489 MW; 75D673729E4C81E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-Jycomb protein E23 (Enhancer of zeste protein 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
  700 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                      Created)
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                                                                                                                                                                                                                                                                                                                                      MEDLINE=99069613; PubMed=9851916;
                                              02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
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Zea mays (Maize).
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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MEDLINE=22357239; PubMed=12467668;
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                                                    SEQUENCE OF 22-82.
                                                                                                                                                                                                                           TISSUE=Venom;
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VARIANT
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                                                                                                                                                                     Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                             Zou C.,
                         7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
       DB 2; Length 895;
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                                                                                                                                                                                                                                 MEDLINE=22751709; PubMed=12815033;
Liang Y. K., Wang Y., Zhang Y., Li S.-G., Lu X.-C., Li H.,
Xu Z.-H., Bai S.-M.,
"OSSETI, a novel SET-domain-containing gene from rice.";
J. Exp. Bot. 54:1995-1996(2003).
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                             Liang Y., Bai S., Xu Z.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407010; AAN01115.1; -.
HSSP; P10968; 7WGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     99800 MW; 47AA0F5DBFB7C84F CRC64;
                                                                                                                                01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                              Grameno; 081LD6; -
GO; GO: 0005634; C: nucleus; IEA.
GO; GO: 0005634; C: nucleus; IEA.
GO; GO: 0005637; F: DNA binding; IEA.
InterPro; IPR0012015; Myb_DNA_binding.
InterPro; IPR008197; WAP.
InterPro; IRR08197; WAP.
InterPro; IRR08197; WAP.
INTERPRO; IRR08197; WAP.
SWART; SM00317; SET; 1.
PROSITE; PS00317; A INSULFIDE_CORE; UNKNOWN 1.
PROSITE; PS00317; A INSULFIDE_CORE; UNKNOWN 1.
PROSITE; PS00317; A INSULFIDE CORE; UNKNOWN 1.
SEQUENCE 895 AA; 99800 MW; 47AAOF5DBFB7C84F CI
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                                                     34.1%; Score 67.5; DB 2; 45.7%; Pred. No. 8.1;
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                                         2 YNLCIRECESICGADGAC---WTWCAD--GCSRSC
      Score 67.5; D
Pred. No. 8.1;
3; Mismatches
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                                                                                                         PRT;
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      ch 34.1%;
1 Similarity 45.7%;
16; Conservative
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                                                                                                        PRELIMINARY;
     Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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SIX2_LELQU
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DT 02-FEB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Zaki T.I., Maruniak J.E.;
"Three polymorphic genes encoding a depressant toxin from the Egyptian scorpion Leiurus quinquestriatus quinquestriatus.";
Toxicon 41:109-113(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-918449, PubMed=2311768,
Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M.,
Rochat H., Granier C.;
"Prinary structure of scorpion anti-insect toxins isolated from the
venom of Leiurus quinquestriatus quinquestriatus.";
PEBS Lett. 261:423-426(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Venom;
MEDLINE=91230120; PubMed=2029523;
Zlotkin E., Eitan M., Bindokas V.P., Adams M.E., Moyer M.,
Burkhart W., Fowler E.;
"Functional duality and structural uniqueness of depressant insect-selective neurocoxins.";
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Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
Polymorphism; Signal; Sodium channel inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93160530; PubMed=8431601;
Zlotkin E., Gurevitz M., Fowler E., Adams M.E.;
"Depressant insect selective neurotoxins from scorpion venom:
Chemistry, action, and gene cloning.";
Arch. Insect Biochem. Physiol. 22:55-73(1993).
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InterPro; IPR002061; Scorpion toxinL.
Pfam; PF00537; Toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ochemistry 30:4814-4821(1991).
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                                                                                                                                                                                                                           Hemocytin precursor (Humoral lectin).
Bombyx mori (Silk moth).
Bukaryota; Wetazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
WCBI_TAXID=7091;
                                                                                                                                                                                                                                                                                                                            STRAIN=Fuyou X Tokai; TISSUE-Hemocyte;
MEDLINE=95178544; PubMed=7873598;
Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M., Matsubara F., Taniai K., Kadono-Okuda K., Kato Y., Mori H.,
"Cloning and expression of the gene of hemocytin, an insect humoral lectin which is homologous with the mammalian von Willebrand factor.";
Biochim. Biophys. Acta 1260:245-258(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolysis.
--- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
--- SIMILARITY: Contains 2 P5/8 type C domains.
--- SIMILARITY: Contains 2 VWFC domains.
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Journal (JAN-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive protein and relates to hemostasis or encapsulation of foreign substances for self-defense.
-!- DEVELOPMENTAL STAGE: Expressed in hemocytes during larval-pupal
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2221-3133 FROM N.A.
Kotani E., Iwamoto S.I., Tashiro M., Mori H., Sumida M., Matsubara
Yamakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: Hemagglutination activity is increased by bacterial viral infection and inhibited by D-mannose, N-acetyl-D-galactosamine and D-maltose.

PTM: May be converted into the 260 kDa mature hemocytin by
                                                                              ;
                                                       Score 67; DB 1; Length 82;
Pred. No. 1.1;
N -> D.
S -> A.
D -> E.
F13D53B18CDECBF0 CRC64;
                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                 PRT; 3133 AA
                                                                            3; Mismatches
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EMBL; D14035; BAA03124.1; -.
PIR; S52093; S52093.
HSSP; P00451; 11QD.
INTERPRO; IPR002919; Cysrich TIL.
INTERPRO; IPR006207; Cys knot_C.
INTERPRO; IPR000491; FASB C.
INTERPRO; IPR0009919; Gal_Bind_like.
INTERPRO; IPR0009919; Gal_Bind_like.
INTERPRO; IPR001007; VWF_C.
                                                                                                  5 CIRECESICGADGACWTW 22
                                                                                                                CNKECKSYGGSYGYCWTW 59
43 43 1
48 48
71 71 1
82 AA; 9099 MW; 1
                                                      33.8%;
55.6%;
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Matches 10; Conserv
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Pfam; PP00754; F5_F8_type_C; 2.
Pfam; PP01826; TIL; 6.
Pfam; PP01826; TIL; 6.
PROSITE; PS012185; CTCK_2; 1.
PROSITE; PS01285; CTCK_2; 1.
PROSITE; PS01286; PA58C_1; 2.
PROSITE; PS01286; PA58C_2; 2.
PROSITE; PS01208; VWFC_1; FALSE_NEG.
Cell adhesion; Glycoprotein; Repeat; Signal.
SIGNAL ? 3133 Hemocytin.
CHAIN ? 3133 Hemocytin.
                                                                                                                                                                                    C-TYPE LECTIN (ATYPICAL)
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POly-Thr.
Poly-Glu.
Poly-Thr.
Poly-Thr.
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RESULT 11

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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatbu M., Hanagaki T., Haraoka T., Hirozane T., A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Ratoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Raito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasto R., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Shibited (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-E57BL/G0; TISSUE=Parthenogenote;
MEDLINE-20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
  Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130034E13 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Parthenogenote;

MEDIANE=20530913; PubMed=11076861;

MEDIANE=20530913; PubMed=11076861;

Schibate K., Itoh M., Mishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamanoto R., Matsunato H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Parthenogenote;
MEDLINE=21085660; PubMed=11217851;
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                                                                       Mus musculus (Mouse).
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Best Local Similarity
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                                                                                                                                     NCBI_TaxID=10090;
                                                    insert sequence
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21330246; PubMed=11437247; DOI=10.1023/A:1010664704926; Vancosthuyse V., Miege C., Dumas C., Cock J.M.;
"Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the male component of the self-incompatibility response."; Plant Mol. Biol. 46:17-34(2001).
-!- TISSUE SPECIFICITY: Expressed in flower buds, but not in stems, roots or rosette leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequer
features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
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05-JUL-2004 (Rel. 44, Last annotation update)
Low-molecular-weight cysteine-rich protein LCR1 precursor.
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                                                                                                                                                                89 AA
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  31
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YNLCIRECESICGADGACWTWCADGCSRSC
                          31 YN--VKECELSC-TGGQQYTVCADSCLRKC
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IDENTIFICATION, AND TISSUE SPECIFICITY.
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                                                                                                                                                                                                           05-JUL-2004 (Rel. 44, Created)
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                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clones.";
DNA Res. 7:31-63(2000).
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01-MAR-2003
01-MAR-2003
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RESULT 12 Q8BRC8 ID Q8BRC AC Q8BRC DT 01-MA DT 01-MA

Matches

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STRAIN=Berkley;
Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Clampe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AA; 64870 MW; D08400487404CFE8 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
LD02520p (Fragment).
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                                                          InterPro; IPR003599; Ig c2.
InterPro; IPR0013599; Ig c2.
InterPro; IPR0010909; PLAC.
InterPro; IPR008123; Prot_Inh_Kunz-m.
InterPro; IPR008197; MAP.
Pfam; PF00047; ig; 3.
Pfam; PF00095; WAP; 1.
                                                                                                                                                                                                                                       PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00059; BASICPTASE.
ProDom; PD000222; Prot_Inh_Kunz-m; 1.
SMART; SM00409; IG; 3.
SMART; SM00408; IGc2; 3.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00317; 4 DISULFIDE CORE; 1. PROSITE; PS00280; BPTI KUNITZ 1; 1. PROSITE; PS50279; BPTI KUNITZ 2; 1. PROSITE; PS00022; EGF 1; UNKNÖMN 1. PROSITE; PS50835; IG_IKK; 3.
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                                      Ig-like.
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PROSITE; PS00022; EGF_1; U
PROSITE; PS50835; IG_LIKE;
PROSITE; PS50900; PLAC; 1.
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SEQUENCE
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AAR82794;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%; Score 65; DB 2; Length 838; 46.2%; Pred. No. 15;
Indels
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-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; BT011127; AAR82794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF07639; YTV; 5.
PROSITE; PS00198; 4FEAS FERREDOXIN; UNKNOWN 1.
Complete proteome; Hypothetical protein.
SEQUENCE 838 AA; 92235 MW; 84AD168706763544 CRC64;
                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
BmBL; BX294146; CAD75374.1; -.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR011521; YTV.
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches 13;
                                                                                                                                                                                                                        838 AA
                                             1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                            10 CVCVCVCVCVCVCVCARACDRYCSHACARYC 40
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 CGGCASSCGSCSACTASCGDGCGSS 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
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9
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Best Local Similarity 46.29
Matches 12, Conservative
10; Conservative
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Rhodopirellula baltica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain 1
                                                                                                                                                                                                                     Q7UNP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6NP04
Matches
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Gaps

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Indels

8

2; Length 591;

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Job time : 186.83 secs

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; Search time 51.283 Seconds (without alignments) 62.956 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                     November 16, 2004, 14:09:48

    protein search, using sw model

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seq length: 200000000
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57
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                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                       Perfect score:
Sequence:
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08
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A\_Geneseq\_23Sep04:\* 1: qeneseq\_1006: geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* •• Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abg60448 Selective	Abr56860 Aminopept	Abg60452 Selective	Abr56864 Aminopept	Abg60450 Selective	Abr56862 Aminopept	Aag74702 Human col	_	Abg70171 Human pre	6 Human	Aaw13427 Breast tu	Aaw60290 Breast ca	Aaw93627 Breast tu	Aab17959 Integrin-	Aab17923 VEGF anta	Aab21702 Human bre	Aae06280 Human bre	Aau81104 Integrin-		_		Adj51706 CH1 delet	Huma	Abb57419 Human sec	Ada98407 Human sec
ΩI	ABG60448	ABR56860	ABG60452	ABR56864	ABG60450	ABR56862	AAG74702	AAM38740	ABG70171	AAM40526	AAW13427	AAW60290	AAW93627	AAB17959	AAB17923	AAB21702	AAE06280	AAU81104	ABB72956	ADJ73110	ADJ52745	ADJ51706	AAE03911	ABB57419	ADA98407
DB	2	9	ഹ	9	ß	9	4	4	'n	4	N	~	~	m	m	m	4	ഹ	ß	7	œ	œ	4	Ŋ	9
Length	6	6	13	13	31	31	28	460	501	512	13	13	13	13	13	13	13	13	13	13	13	13	43	43	43
& Query Match	100.0	100.0	87.7	87.7	82.5	82.5	77.2	75.4	75.4	75.4	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	•	70.2	•	70.2	70.2
Score	57	57	20	20	47	47	44	43	43	43	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
Result No.	-	7	М	4	ß	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Human Human Human Human Human Human Human Human Human Human Human Human Human	Aau01069 Human sec Aau01949 Human sec Aab60747 Human sec Ade11750 Human sec
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44444444444444444444444444444444444444	40 70.2 40 70.2 40 70.2 40 70.2
6 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 5 6 4 5

## ALIGNMENTS

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; Selective targeting peptide #123. ABG60448 standard; peptide; 9 AA. (first entry) gene therapy. 30-JUL-2002 ABG60448; 

Synthetic.

WO200220769-A1.

14-MAR-2002.

07-SEP-2001; 2001WO-US027692

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R; Arap W, WPI; 2002-415731/44

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular disease.

Claim 22; Page 102; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

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Indels

Length 9;

100.0%; Score 57; DB 6; I 100.0%; Pred. No. 1.7e+06; iive 0; Mismatches 0;

Conservative

Local Similarity

Best Loc Matches

Query Match

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ABG60452 standard; peptide; 13 AA.

ABG60452

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Selective targeting peptide #127.

(first entry)

30-JUL-2002

ABG60452;

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for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60316-ABG60574 represent selective targeting peptides of the invention
inflammation or macular degeneration. Furthermore, the peptide is useful
                                                                                                                                                                                                                                                                                                                                                                Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta. integrin; beta.5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
                                                                                                                                            Gaps
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0
                                                                                                                                           Indels
                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                         Aminopeptidase A (APA) binding peptide SEQ ID NO:56.
                                                                                                                100.0%; Score 57; DB 5; I 100.0%; Pred. No. 1.7e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasqualini R, Arap W, Kolonin MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 98; 247pp; English.
                                                                                                                                                                                                                                                             ABR56860 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2002; 2002WO-US027836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                           Conservative
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                                                                                                                                                                                              CPRECESIC 9
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                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                    CPRECESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating obesity
peptide selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003022991-A2
                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                               30-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                       ABR56860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subject.
                                                                                                                                        Matches
                                                                                                                                                                                                                                              RESULT 2
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Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; acardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;

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The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmume disease, bacterial infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foctus, by attaching subject. Sequences ABG60326-ABG60574 represent selective targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 5
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subject. Sequences ABG6032 peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPRECESIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA;
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Matches
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The present invention describes a method for treating obesity or a selective for adipose tissue; (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and dispose targeting peptides have anorectic and antilipaemic activities, and can be used in peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immundeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABRS6806 to ABRS6827 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention

Sequence 9 AA;

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune disease, infections or cardiovascular

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

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Arap W, Pasqualini WPI; 2002-415731/44.

07-SEP-2001; 2001WO-US027692

WO200220769-A1

Synthetic.

gene

14-MAR-2002.

Claim 22; Page 109; 317pp; English

disease.

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CPRECESNC 13

Selective targeting peptide #125.

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pepčide therapy, gene therapy, infection, human immunodeficiency virus, HIV, placental delivery, teratogenic; placenta, adipose, pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                     Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
                                                                                                           antilipaemic;
                                                                                                        Targeting peptide; obesity; lipodystropathy; anorectic;
                                                                                    Aminopeptidase A (APA) binding peptide SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 104; 247pp; English.
                                                                                                                                                                                                                                                                                             Kolonin MG;
                      ABR56864 standard; peptide; 13 AA.
                                                                                                                                                                                                                              30-AUG-2002; 2002WO-US027836.
                                                                                                                                                                                                                                                   07-SEP-2001; 2001WO-US027692.
                                                                 30-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                            Pasqualini R, Arap W,
                                                                                                                                                                                                                                                                                                                 WPI; 2003-371749/35.
                                                                                                                                                                                    WO2003022991-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13 AA;
                                                                                                                                                                                                         20-MAR-2003
                                                                                                                                                               Synthetic
                                            ABR56864;
                                                                                                                                                                                                                                                                                                                                                                      subject.
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The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic selective form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as also be used for targeting delivery to an organ or tissue, such as consecred addivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for traracogenic activity. ABN558806 to ABN56927 and ACC79101 represent sequences used in the exemplification of the present invention

Gaps ö Score 50; DB 6; Length 13; Pred. No. 1.1; 0; Mismatches 1; Indels 1; Indels 87.78; 88.98; 8; Conservative CPRECESIC 9 Best Local Similarity Matches 8; Conserv Query Match

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ABG60450 standard; peptide; 31 AA. ABG60450; ABG60450 SXXXE

RESULT 5

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(first entry)
 30-JUL-2002
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ö The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with inflammation or macular degeneration. Purthermore, the peptide is useful for diagnosing the disease cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching apptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60126-ABG60574 represent selective targeting Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; antiinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A. Gaps .; 0 DB 5; Length 31; 1; Indels Aminopeptidase A (APA) binding peptide SEQ ID NO:58. Pred. No. 6.3; 0; Mismatches Score 47; Pred. No. 6 Claim 22; Page 108; 317pp; English. Ä ABR56862 standard; peptide; 31 08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US027692 82.5%; 88.9%; (TEXA ) UNIV TEXAS SYSTEM. peptides of the invention (first entry) 8; Conservative CIRECESIC 13 σ WPI; 2002-415731/44. Arap W, Pasqualini 1 CPRECESIC Query Match Best Local Similarity Sequence 31 AA; WO200220769-A1 gene therapy. 30-JUL-2003 14-MAR-2002 Synthetic. ABR56862; disease. Matches ABR56862 RESULT ઠે g 

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The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABR56806 to
                                                                                                                                                                                                                                                   Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 6; Length 31;
Pred. No. 6.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer antigen protein SEQ ID NO:5466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                  Example 8; Page 104; 247pp; English
                                                                                                                                                                                              Kolonin MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG74702 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0157137P.
                                                                                                      30-AUG-2002; 2002WO-US027836.
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                                                                                                                                    07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-2001 (first entry)
                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                              Pasqualini R, Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIRECESIC 13
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                                                                                                                                                                                                                           WPI; 2003-371749/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPRECESIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                           WO2003022991-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999;
03-NOV-1999;
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                                                                         20-MAR-2003
               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG74702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
8
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cancer-associated nucleic acid molecules (N) and proteins the cancer-associated nucleic acid molecules (N) and proteins are collectively known as colon cancer antigens. The colon cancer antigens have evestatic activity and can be used in gene therapy and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P car be used in the prevention, diagnosis and treatment of colorectal sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                     and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB
Pred. No. 29;
1; Mismatches
                                                                                                                                                                                    Claim 11; Page 7070-7071; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM38740 standard; protein; 460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 1885.
                                                   Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US034263
                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 CPRECSFLC 37
                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                                    2001-235357/24
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Best Local Similarity
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                                                                                                   N-PSDB; AAH34107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                   Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM38740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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The invention relates to a complex of protein-protein interactions between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC, ipaH9.84, ospG and ospC1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the Shigella flexneri polypeptide and a mammalian polypeptide and a mammalian polypeptide defined in the specification; (2) selecting a modulating compound obtained from the method of (2); (4) a SID computating compound obtained from the method of (2); (4) a SID comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a SID polypeptides a vector comprising the vector; and (10) a protein chip comprising the vector; and (10) a protein chip comprising the composition of the composition of the composition of the composition of polypeptide or polymucleotide is useful for treating or preventing shigella shigelial structure of the polymucleotide is useful for treating or preventing and a mammalian polypeptide or mammalal. The present control of selection or mammalal. The present control of selection or mammalal. The present control or polymucleotide is useful for mammalal. The present control or protein control or mammalal. The processing the control or properties or protein control or mammalal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a human prey protein isolated by the yeast two-hybrid
                                                                                                            flexneri polypeptide and a prey mammalian or human placenta polypeptide
for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, nootropic, immunosuppressant, cytostatic, gene therapy; cancer, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                            New complex of protein-protein interactions between a bait Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assay, forming a complex of the invention with a shigella protein
                                                                                                                                                                                   Claim 7; Page 116-117; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM40526 standard; protein; 512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 5457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-00471275.
2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.4%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRECEPIC 40
                          WPI; 2002-599706/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRECESIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                               N-PSDB; ABS51564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200153312-A1.
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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM40526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as alzeimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinihinha activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                              Wang D;
, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prey protein, ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
                                                                                                                                                                                                                                                                                                                        nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                              Ren F, Wa
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Pred. No. 2.3e+02;
3; Mismatches 1; Indels
                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                         Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 1885; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prey protein for Shigella ipaH9.8 #1.
                                                                                                                                                                                                                                                                                                                                                  as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG70171 standard; protein; 501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    part of the printed specification
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-0066191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-2001; 2001US-0261130P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                      2001-442253/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                             N-PSDB; AAI57896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 460 AA;
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                                                                                                                                                         YT,
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                                                                                                                                                                                        Wang
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RESULT 9

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Gaps

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Score 43; DB 5; Length 501; Pred. No. 2.4e+02; 0; Mismatches 1; Indels

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This synthetic peptide is a claimed example of a breast tumour-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method trypically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAM1181-52, AAM1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour homing molecules and their conjugates - useful for, e g. directing linked moiety to tumour containing angiogenic vasculature.
                                         Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour homing peptide; in vivo panning; breast carcinoma; alpha-V-containing integrin binding motif; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2; Length 13;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breast carcinoma tumour homing peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 6; 105pp; English
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                                                                                                                             Claim 18; Page 68; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW60290 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                           maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruoslahti E, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPRICOSSC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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    WPI; 1997-202359/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-207151/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                               Ren F, Wang D;
Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast tumour homing peptide; cancer; in vivo panning; screening; phage display; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                           Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.4%; Score 43; DB 4; L
55.6%; Pred. No. 2.5e+02;
ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 5457; 10078pp; English.
                                                                                                                                                                                                                                                                                                      as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13427 standard; peptide; 13 AA.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US014600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast tumour homing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t Local Similarity 55.6
ches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 CPQECPAVC 499
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                                                                                                                                                                                                                WPI; 2001-442253/47.
                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                  N-PSDB; AAI59682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1998
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                                                                                                                                                   Wang J,
Zhou P,
                                                                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches

8

AAW13427

by in vivo panning. The peptide homes to a breat carcinoma. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying epetide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour is not present in the normal tissue. The tumour homing

(LJOL-) LA JOLLA CANCER RES FOUND.

Pasqualini R;

Ruoslahti E,

95US-00526710.

95US-00526708

11-SEP-1995;

11-SEP-1995;

The present peptide represents a tumour homing peptide, and is produced

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Gaps

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Indels

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RESULT 14
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SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying molecules that home to angiogenic vasculature used as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic; anti-athritic; NGR receptor; inhibitor; angiogenesis; anticanner drug; prognosis; inflammation; regeneration; wounded tissue; targetting; macular degeneration; diabetic retinopathy; rheumatoid arthritis;
peptide can be linked to a moiety (e.g. doxorubicin), and used to direct
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel peptides which home to angiogenic
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                                                                                                               Length 13;
                                                                                                                                                              2; Indels
                                                                                                               5;
                                                                                                               DB:
                                                                                                                                                              1; Mismatches
                                                                                                                 Score 40;
                                                                                                                                           Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       AAW93627 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast tumour homing peptide 1.
                                                                                                                 70.2%;
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasqualini
                       the moiety to a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for anticancer agents.
                                                                                                                                                                                                                                                      CPRLCQSSC 13
                                                                                                                                                                                                         1 CPRECESIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-215158/18.
                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          occlusive thrombus
                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1997;
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                                                                                                                 Query Match
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                                                                                                                                                              Matches
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LD AAW8

AAW93627

AAW8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; cytotoxic; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
AAW93843-44 are examples of tumour homing peptides used in the invention
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                                                                                                                              Gaps
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                                                                                                                              2; Indels
                                                                                    Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin-binding peptide sequence SEQ ID NO:1071.
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7
                                                                                  DB
31;
                                                                                                                              1; Mismatches
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                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 589; 608pp; English.
                                                                                                                                                                                                                                                                                                                       AAB17959 standard; peptide; 13 AA.
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99US-00428082.
                                                                                  70.2%;
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                                                                                                                              6; Conservative
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                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                       1 CPRECESIC
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                                             Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                AAB17959;
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The present invention describes composition of matter (I) comprising an Fe domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-PI-(X2)b, where: FI = an Fe domain; XI and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L3)c-P1-(L2)d-P2-(L3)e-P3. or -(L3)c-P1-(L2)d-P2-(L3)e-P3. or -(L3)c-P1-(L2)d-P2-(L3)e-P3. or -(L3)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-F4 where P1, P2, P3-(L4)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-F4 where P1, P2, P3-(L4)c-P1-(L2)d-P3-(L4)f-F4 where P1, P2, P3-(L4)c-P1-(L2)d-P3-(L4)f-F4 where P1, P2, P3-(L4)c-P1-(L3)c-P3-(L4)c-P1-(L3)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L3)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3-(L4)c-P3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                  Gaps
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                                                  ;
  ; DB 3; Length 13;
                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF antagonist peptide sequence SEQ ID NO:1027.
                                                  Mismatches
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  Score 40;
Pred. No. 3
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                                                                                                                                                                                                                                                                      AAB17923 standard; peptide; 13 AA.
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99US-00428082.
70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                  Conservative
                                                                                                                                              CPRLCQSSC 13
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  Query Match
Best Local Similarity
                                                                                                1 CPRECESIC
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                         Best Loc
Matches
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Score 40; DB 3; Length 13; Pred. No. 31;

70.2%; 66.7%;

Query Match Best Local Similarity

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 Gaps
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 2; Indels
 1; Mismatches
                                                                                      Search completed: November 16, 2004, 14:24:26 Job time : 59.283 secs
 6; Conservative
                                                 s čPRLČQSSC 13
                         1 CPRECESIC 9
 Matches
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us-10-784-537-2.rai

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Best Local Similarity
Matches 6; Conserv
US-09-139-802-2
 LENGTH: 13
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                                                                                                                                                                                                                                                     RESULT 1
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Sequence 2, Appli
Sequence 2, Appli
Sequence 1071, Ap
Sequence 1071, Ap
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 27, Appl
Sequence 196, Appl
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                         ; Search time 12.7358 Seconds (without alignments)
46.865 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-926-914-2

US-09-270-767-42488

US-09-270-767-42488

US-09-270-767-42488

US-09-252-914-26031

US-09-055-699-37

US-09-055-699-37

US-09-661-468-37

US-09-661-468-37

US-09-61-468-37

US-09-61-468-37

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US-08-97-196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-153-927-2
US-09-565-918-5
                                                                                                                                                                                               478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                           2004, 14:16:01
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                 US-10-784-537-2
57
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Match Length DB
                                                                                                                                          1 CPRECESIC 9
                                                                           November 16,
                                                                                                                                                                 BLOSUM62
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                                                                                                                     Title:
Perfect score:
                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                            Sequence:
                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                     Database
                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
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GENERAL INFORMATION:
APPLICANT: Rauslahti, Erkki
APPLICANT: Rauslahti, Erkki
APPLICANT: Rausqualini, Renate
ITILE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
ITILE OF INVENTION: Same
ITILE OF INVENTION: Same
FILE REPERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
MUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.2
                                   Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1,  Appli
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Sequence 2, Application US/09659786

Sequence 2, Application US/09659786

Sequence 2, Application US/09659786

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erki

APPLICANT: Rasqualini, Renata

TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

FILLE REPERENCE: P-LJ 3200

FILLE REPERENCE: P-LJ 3200

CURRENT APPLICATION NUMBER: US/09/659,786
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Sequence 10,
                Sequence
Sequence
Sequence
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US-09-139-802-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                   US-09-557-908-4
US-09-813-966-4
US-08-813-966-4
US-08-813-966-2
US-09-557-908-2
US-09-533-966-2
US-09-546-553-2
US-09-134-000C-5543
US-09-134-000C-5543
US-09-138-958-5
US-09-538-092-206
US-08-537-210A-1
US-08-113-825-1
US-08-113-825-1
US-08-113-825-1
US-08-113-825-1
US-08-113-825-1
US-08-113-825-1
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Patent No. 6180084
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ORGANISM: Artificial Sequence
                                        417
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428
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859
11015
12015
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CPRLCQSSC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-09-659-786-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                         Mismatches
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FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PATCHLIN Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08926914
Patent No. 6576239
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 13 amino acids TYPE: amino acid
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MOLECULE TYPE: peptide
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5 CPRLCQSSC 13
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Matches 6; Conserv
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                                                                                                                                        LENGTH: 13
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: U5/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-05-270-767-42488

Sequence 42488, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1998-03-17

NUMBER OF SEQ ID NOS: 62517
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                          sequence 10.1, Application US/U9428082B
Fatent No. 6660843
GENERAL INFORMATION:
APPLICANT: FIELS, ULAICH
APPLICANT: CHEETHAM, JANET C.
APPLICANT: CHEETHAM, JANET C.
FILE REFRENCE: A-5.7
FILE REFRENCE: A-5.7
FILE REFRENCE: A-5.7
FILE REFRENCE: A-5.7
FILE REPRENCE: A-5.7
FILE REPRENCE: A-5.7
FILE REPRENCE: A-5.7
FILE OF INVENTION: NUMBER: US/09/428,082B
CURRENT APPLICATION NUMBER: 06/105,371
FRIOR APPLICATION NUMBER: 60/105,371
FRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
FUNDE: 100 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 4; Length 13;
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-09-428-082B-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                     ; Sequence 1071, Application US/09428082B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.2%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-57784
US-09-428-082B-1071
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                                                                                                                                                                                                                                                                          Length 816;
                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                       70.2%; Score 40; DB 2; I 66.7%; Pred. No. 2.7e+02; tive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Takeshi, WATANABE
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KATAGIRI
ITILE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application US/09055699 Patent No. 6005088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEX: (202) 293-7660
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
                                                                           TELEX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
                                           (202) 293-7060
(202) 293-7860
                                                                                                                                          : 816 amino acids
amino acid
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TYPE: amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-170A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-055-699-37
                                                                                                                                                                                                                                                                                                                                                                                      326 CCKECKSIC 334
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                                         TELEPHONE:
TELEFAX: (
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US-09-055-699-37
                                                                                                                                                                                                                                                                              Query Match
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Sequence 26031, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBENCE: 136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26031

LENGTH: 596
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GENERAL INFORMATION:
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: Toyomaaa, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: SUGHTHE, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 4; I
Pred. No. 2.1e+02;
1; Mismatches 1;
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                                                                                ; ORGANISM: Drosophila melanogaster
US-09-270-767-42488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26031
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Best Local Similarity 75.0%;
Matches 6; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42488
LENGTH: 118
                                                                                                                           Query Match
Best Local Similarity 66./-
6, Conservative
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. Sequence 37, Application US/09976165 . Patent No. 6562947
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Best Local Similarity 66.7%;
Matches 6; Conservative 7
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                                            326 CCKECKSIC 334
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ORGANISM: Homo sapiens
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1 CPRECESIC 9
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Patent No. 6333404

GENERAL INFORMATION:
PAPELICANT: FULINGRAP, TSUTOMU
PAPELICANT: HORIE, MASATO

TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: MUMBER: US/09/565,538

CURRENT APPLICATION NUMBER: US/09/565,538

CURRENT PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1997-03-19

PRIOR PILING DATE: 1997-03-05

                                           Sequence 37, Application US/09273565A

Sequence 37, Application US/09273565A

Patent No. 6166190

GENERAL INFORMATION:
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

TITLE OF INVENTION: AN USOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

TITLE OF INVENTION: SKELFTAL MUSCLE-SPECIFIC UBIQUITIN-CONUUGATING ENZYME

FILE REFERENCE: Q-53599

CURRENT PRILING DATE: 1999-03-22

EARLIER APPLICATION NUMBER: 09/055,699

EARLIER APPLICATION NUMBER: 08/820,170

EARLIER APPLICATION NUMBER: JP 63410/1996

EARLIER PILING DATE: 1997-03-05

NUMBER OF SEQ ID NOS: 95

SEQ ID NO 37

LENGTH BACT

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Best Local Similarity 66.79
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-273-565-37
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LENGTH: 816
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GABRIAL INFORMATION:

APPLICANT: WATANABE, TSUTOWU

APPLICANT: WATANABE, TAKESHI

APPLICANT: WATANABE, TAKESHI

APPLICANT: HORIE, MASATO

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

FILE REFERENCE: 0-5359

CURRENT APPLICATION NUMBER: US/09/661,468

CURRENT PILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1997-03-19

PRIOR FILING DATE: 1997-03-19

PRIOR FILING DATE: 1997-03-19

PRIOR FILING DATE: 1997-03-05

PRIOR PRIOR APPLICATION NUMBER: UP 69163/1997

PRIOR FILING DATE: 1997-03-05

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PARCENTI OF 10 NOS: 95

LENGTH: 816
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APPLICANT: FULWARA, TSUTOWU
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REPERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/976,165
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-04-07
PRIOR PELLING DATE: 1998-04-07
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-05
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH B16
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Pred. No. 2.7e+02;
2; Mismatches 1; Indels
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ORGANISM: Homo sapiens
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Sequence 5457, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
TITLE OF INVENTION: UNMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5457
LENGTH: 723
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Sequence 995, Application US/09538092

Sequence 995, Application US/09538092

Sequence 995, Application US/09538092

Sequence 995, Application US/09538092

SEXERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT FILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTMARE: CurapatSegFormatter Version 0.9

SEQ ID NO 995

LENGTH: 699

LENGTH: 699
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Score 40; DB 4; Length 816;
Pred. No. 2.7e+02;
2; Mismatches 1; Indels
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Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels
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; NAME/KEY: misc_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number P23327

US-09-538-092-995
  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 2
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ORGANISM: Proteus mirabilis
US-09-543-681A-5457
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Best Local Similarity 66.7
Matches 6; Conservative
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665 CPLVCETVC 673
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ORGANISM: Homo sapiens
FEATURE:
                                                                                             1 CPRECESIC 9
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Job time : 14.0692 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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75.615 Million cell updates/sec
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1: \( \cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubCoMB} \( \text{.ppp} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{PubCoMB} \( \text{.ppp} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{Pubpa} \( 1\) \text{NEW} \\ \text{PUBCOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{Pubpa} \( 1\) \text{NEW} \\ \text{.pub} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pub} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pub} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pub} \\ \text{.pubpa} \\ \text{.pubCOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pub} \\ \text{.pubpa} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEOMB} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pep} : \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pep} : \text{.lg} \\ \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{NEW} \\ \text{.pep} : \text{.lg} \\ \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \\ \text{.pep} : \text{.lg} \\ \text{.cgn2} \frac{6}\) \text{prodata} \( 1\) \\ \text{pubpa} \( 1\) \\ \text
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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Maximum DB 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                      Run on:
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Description	Sequence 123, App	Sequence 127, App	Sequence 125, App	Sequence 5476, Ap	Sequence 521, App	Sequence 206937,	Sequence 2, Appli	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 1071, Ap	Sequence 1071, Ap	Sequence 1071, Ap
ID	US-10-363-204-123	US-10-363-204-127	US-10-363-204-125	US-10-106-698-5476	US-10-043-487-521	US-10-424-599-206937	US-09-765-086-2	US-09-840-277-32	US-10-264-374-2	US-10-375-992-2	US-10-609-217-1071	US-10-632-388-1071	US-10-651-723-1071
OB	16	16	16	14	14	12	σ,	0	14	14	12	15	15
Length	6	13	31	28	89	102	13	13	13	13	13	13	13
Query Match	100.0	87.7	82.5	77.2	75.4	71.9	70.2	70.2	70.2	70.2	70.2	70.2	70.2
Score	57	50	47	44	43	41	40	40	40	40	40	40	40
Result No.		7	e	4	S	9	7	80	6	10	11	12	13
	Query Score Match Length DB ID	Ouery Score Match Length DB ID 57 100.0 9 16 US-10-363-204-123	Ouery Score Match Length DB ID 57 100.0 50 87.7 13 16 US-10-363-204-123	Core Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-127 47 82.5 31 16 US-10-363-204-125	Query       Score Match Length DB ID       57 100.0     9 16 US-10-363-204-123       50 87.7     13 16 US-10-363-204-127       47 82.5     31 16 US-10-363-204-127       47 82.5     31 16 US-10-363-204-125       44 77.2     58 14 US-10-106-688-5476	Acore Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-127 47 82.5 31 16 US-10-363-204-125 44 77.2 58 14 US-10-06-698-5476 43 75.4 89 14 US-10-043-489-521	Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-127 47 82.5 31 16 US-10-363-204-125 44 77.2 58 14 US-10-363-204-125 43 77.2 58 14 US-10-043-487-521 41 71.9 102 15 US-10-424-599-206937	Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-127 47 82.5 31 16 US-10-363-204-125 44 77.2 58 14 US-10-06-698-5476 43 75.4 89 14 US-10-06-698-5476 43 75.4 89 14 US-10-0424-599-206937 40 70.2 13 9 US-09-765-086-2	Acore Match Length DB ID  Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 58 87.7 13 16 US-10-363-204-125 44 77.2 58 14 US-10-106-698-5476 43 75.4 89 14 US-10-106-698-5476 44 77.9 102 15 US-10-043-487-521 40 70.2 13 9 US-09-640-277-32	Acore Match Length DB ID  Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-125 44 77.2 53 14 US-10-363-204-125 44 77.2 58 14 US-10-043-487-521 41 71.9 102 15 US-10-043-487-521 40 70.2 13 9 US-09-765-086-2 40 70.2 13 9 US-09-76-377-32 40 70.2 13 14 US-10-264-377-3	Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 59 82.5 31 16 US-10-363-204-127 47 82.5 31 16 US-10-363-204-127 44 77.2 58 14 US-10-363-204-125 44 77.2 58 14 US-10-043-497-521 41 71.9 102 15 US-10-043-497-521 40 70.2 13 9 US-09-765-086-2 40 70.2 13 14 US-10-264-374-2 40 70.2 13 14 US-10-375-992-2	Acore Match Length DB ID  Score Match Length DB ID  57 100.0 9 16 US-10-363-204-123 50 87.7 13 16 US-10-363-204-125 47 82.5 31 16 US-10-363-204-125 44 77.2 58 14 US-10-106-698-5476 43 75.4 89 14 US-10-106-698-5476 40 70.2 13 9 US-09-840-277-3 40 70.2 13 14 US-10-277-3 40 70.2 13 14 US-10-375-992-2 40 70.2 13 14 US-10-375-992-2 40 70.2 13 14 US-10-375-992-2 40 70.2 13 15 US-10-375-992-2	Acore Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Length DB ID  Match Identification  Match Identi

RESULT 2
US-10-363-204-127
Sequence 127, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:

Sequence 1071, Ap Sequence 1071, Ap Sequence 1071, Ap Sequence 2, Appli Sequence 2, Appli	38228	Sequence 828, App Sequence 375, App Sequence 764, App Sequence 2, Appli	Sequence 5569, Ap Sequence 13717, A Sequence 12163, A Sequence 44382, A	m	Sequence 8, Appli Sequence 300117, Sequence 168031, Sequence 168031,	Sequence 21251, A Sequence 434, App Sequence 346, App Sequence 27, Appl
15 US-10-645-761-1071 15 US-10-666-696-1071 15 US-10-653-048-1071 15 US-10-264-374-2 16 US-10-375-992-2	17 US-10-425-115-220960 10 US-09-948-783-122 10 US-09-892-877-121 11 US-10-425-115-364176 14 US-10-263-828-79	15 US-10-112-944-828 15 US-10-112-944-375 9 US-09-764-868-764 15 US-10-168-618A-2	9 US-09-815-242-5569 14 US-10-156-761-13717 9 US-09-815-242-12163 15 US-10-282-122A-44382	15 US-10-282-122A-63642 10 US-09-901-136-4 10 US-09-901-136-2 15 US-10-108-260A-3263 16 US-09-976-16-37		14 US-10-369-493-21251 16 US-10-408-765A-434 14 US-10-369-493-346 9 US-09-765-086-27
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700.2	00000	20.07	20.07	200000	68.2 68.4 68.4 68.4 68.4	68.4 68.4 66.7
4444	4444	4444	444	44444	4 6 6 6 6 5 0 0 0 0	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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## ALIGNMENTS

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Sequence 123, Application US/10363204

Sequence 123, Application US/10363204

Publication No. US20040170955A1

GENERAL INFORMATION:

APPLICANT: Board of Regents, The University of Texas System

TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT

CURRENT APPLICATION NUMBER: US/10/363,204

CURRENT FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 251

SOFTWARE: Patentin version 3.1

SEQ ID NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 57; DB 16;
100.0%; Pred. No. 1.4e+06;
attive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
LOCATION: (1)..(9)
CTHER INFORMATION: synthetic construct
US-10-363-204-123
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
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US-10-363-204-123
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APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein interactions between Shigella Flexneri polypeptide
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US 10/043, 487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin Version 3.1
SEQ ID NO 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 206937, Application US/10424599

Sequence 206937, Application US/10424599

Sequence 206937, Application No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 206937

TYPE: PRT

CRARTISM: Glycine max
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                                                                                                                                                                                       Score 44; DB 14; Length 58;
Pred. No. 25;
1; Mismatches 2; Indels
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_28891C.1.pep
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Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 521, Application US/10043487
Publication No. US20030055220A1
GENERAL INFORMATION:
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ORGANISM: Shigella Flexneri
                                                                                                                                                                    Query Match
Best Local Similarity 66.7
اتم 6، Conservative
       NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5476
LENGTH: 58
                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5476
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide
FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT PILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/1000/26524
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-363-204-125

Sequence 125, Application US/10363204

Publication No. US20040170955A1

GENERAL INFORMATION:

APPLICANT: Board of Regents, The University of Texas System

TITLE OF INVENTION:

FILLE REFERENCE: 005774-P003PCT

CURRENT APPLICATION NUMBER: US/10/363,204

CURRENT FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 251

SOOTWARE: Patentin version 3.1

SEQ ID NO 125

LENGTH: 31
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILLE REPERENCE: 005774-1003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILLING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFFWARE: PatentIn version 3.1
SEQ ID NO 127
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88.9%; Pred. No. 1;
ative 0; Mismatches 1; Indels
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88.9%; Pred. No. 5.6;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
US-10-363-204-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5476, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.5
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                              TYPE: PRT
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APPLICANT: Rucelahti, Erkki
APPLICANT: Rucelahti, Renata
Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide
US-10-264-374-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 14; Length 13;
Pred. No. 28;
1; Mismatches 2; Indels
                Score 40; DB 9; Length 13;
Pred. No. 28;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ANDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/375,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/10375992; Publication No. US20030152578A1; GENERAL INFORMATION:
                70.2%;
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 66.
المام 6. Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                      5 CPRLCQSSC 13
                                                                                                1 CPRECESIC 9
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US-10-375-992-2
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                                      Query Match 71.9%; Score 41; DB 15; Length 102; Best Local Similarity 55.6%; Pred. No. 1.1e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                            APPLICANT: ACCOUNT AND ACCOUNTS. APPLICANT: Madih, Arap APPLICANT: Wadih, Arap APPLICANT: Bredesen. Dale B. APPLICANT: Bredesen. Dale B. TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With TITLE OF INVENTION: Day 4400 process and Application NUMBER: US/09/765,086 CURRENT FILING DATE: 2001-01-17 PRIOR PEPLICATION NUMBER: US 09/489,582 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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Sequence 3.2 Application US/09840277

GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LES
TITLE OF INVENTION: INFEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 06/198,919
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 32

SEQ ID NO 32
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Pred. No. 28;
1; Mismatches
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; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: synthetic peptide US-09-765-086-2
                                                                                                                                                                                                                                                    Sequence 2, Application US/09765086
Patent No. US200100046498A1
GENERAL INFORMATION:
APPLICANT: RUOSIANT, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 6; Conservative
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  US-10-424-599-206937
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US-09-765-086-2
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APPLICANT: CHEETHAM, JANET C.

APPLICANT: BOONE, THOMAS CHARLES

TITLE OF INVENTION: WODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-52.

CURRENT APPLICATION NUMBER: US/10/632,388

CURRENT APPLICATION NUMBER: US/09/428,082B

PRIOR APPLICATION NUMBER: US/09/428,082B

PRIOR FILING DATE: 1999-10-22

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PATCHING UN OFFEINS 3.1

SEQ ID NO 1071
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APPLICANT: LIU, CHUAN-FA
APPLICANT: CHETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
ITTLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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COTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR PILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-651-723-1071
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Publication No. US20040071712A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1071, Application US/10651723
; Publication No. US20040057953A1
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Fublication No. US20040044188A1
GENERAL INFORMATION:
APPLICANT: ETGE, ULEICH
APPLICANT: LIU, CHUAN-FA
FIREMENT: LIU, CHUAN-FA
FILEMETHAM: JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT FILING DATE: 2003-06-27
FRIOR APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 1999-10-22
FRIOR APPLICATION NUMBER: 05/105,371
FRIOR PILING DATE: 1999-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                ATTORNEY, AGENT INFORMATION:
ATTORNEY, AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: both
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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FILING DATE: 27-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acid
TYPE: amino acid
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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5 CPRLCQSSC 13
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LENGTH: 13
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; Publication No. US20040077022A1
; GENERAL INFORMATION:
    APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FR
; APPLICANT: CHESTHAM, JANET C.
    APPLICANT: GUDAS, USAN MARIE
; APPLICANT: GUDAS, USAN WARIE
; TITLE OP INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; PILE REFERENCE: A-5-7A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-23
; PRIOR FILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 1157
; SEQ ID NO 1071
; LENGTHAN : 13
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HILE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/645,761
CURRENT PILING DATE: 2003-08-18
FRIOR APPLICATION NUMBER: US/09/428,082B
FRIOR APPLICATION NUMBER: 00/105,371
PRIOR FILING DATE: 1998-10-22
FRIOR PILING DATE: 1998-10-23
FRIOR FILING DATE: 1998-10-23
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Job time : 44.1132 secs
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 66.7
Matches 6; Conservative
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5 CPRLCQSSC 13
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5 CPRLCQSSC 13
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67.889 Million cell updates/sec
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2: (cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: (cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
8: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
11: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
12: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
14: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
15: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
16: (cgn2_6/ptodata/1/paa/US084_COMB.pep:*
17: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
18: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
19: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
19: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
10: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
11: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
12: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
13: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
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10: (cgn2_6/ptodata/1/paa/US094_COMB.pep:*
10: (cgn2_6/
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               - protein search, using sw model
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57
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Sequence 56, Appl	12		Sequence 127, App	Sequence 60, Appl	Sequence 127, App	Sequence 3, Appli	Sequence 125, App	ω̈́	~	1,	o,	'n	14	5466, A	5476,	521,	1885,	1885,	1885,		5457,	5457,	1223,		12244	Sequence 206937,	equence 1877, A	1876,	8831				Sequence 303;	1875,	290, 7	e 589	Sequence 2, Appli		_	'n	ď	7	107
QI	PCT-US01-27692A-123	Д	6	m		Д	6	m	PCT-US01-27692A-	PCT-US02-27836-58	9 US-10-363	US-10-784			3 US-10-784-537-6	PCT-US00-2	7 US-10-106	6 US-10-043	80	8 US-10-258	8 US-10-286	60	80	80	N	80	80	0	PCT-US99-22853B-1877	O.	US-09-724-676-8831			21 US-09-724-676A-88324		PCT-US99-22853B-1875	6 US-60-550-051-29	9		PCT-US99-25044-1027	PCT-US99-25044-1071	US-08	-09-23	8 US-09-489-582-2	9 US-09-563-286B-1071
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Query	100.0	100.0	100.0	100.0	87.7	87.7	87.7	87.7	82.5	82.5	82.5	82.5	82.5	77.2	77.2	77.2	77.2	75.4	75.4	75.4	75.4	75.4	75.4	75.4	71.9	71.9	71.9	71.9	71.9	71.9	71.9		٠	٠	71.9	71.9	71.9	71.9	70.2	70.2	70.2	70.2	70.2	70.2	70.2
Score	57	57	57	57	20	20	20	20	47	47	47	47	47	44	44	44	44	43	43	43	43	43	43	43	41	41	41	41	41	41	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40
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## ALIGNMENTS

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PCT-US01-27692A-123
; Sequence 123, Application PC/TUS0127692A
; Sequence 123, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; TILE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)...(9)
; OTHER INPORMATION: synthetic construct
PCT-US01-27692A-123
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APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REPERENCE: 005774.2003BCT
CURRENT APPLICATION NUMBER: PCT/US01/27692A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 13
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                                                                                                                                                                                                       | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John Company | John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Score 50; DB 1; Length 13; Similarity 88.9%; Pred. No. 2.2; 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i LOCATION: (1)..(13)
i OTHER INFORMATION: synthetic construct
PCT-US01-27692A-127
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OOGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Peptide
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 8; Conserva
                                              1 CPRECESIC
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FILE REFERENCE: 5774, P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
CURRENT FILING DATE: 2002-08-30
FRIOR APPLICATION NUMBER: PCT/US01/27692
FRIOR APPLICATION NUMBER: PCT/US01/27692
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
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TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.0039CT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.1
SEQ ID NO 123
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: Durposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                    Length 9;
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                   100.0%; Score 57; DB 1; L illarity 100.0%; Pred. No. 6.2e+06; Conservative 0; Mismatches 0:
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; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-204-123
                                                                                                                                                                                                                                                                                                                         RESULT 2
PCT-0802-27836-56
PSequence 56, Application PC/TUS0227836
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity الاس
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Query Match
Best Local Similarity
9; Conserv?
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PCT-US01-27692A-125

Sequence 125, Application PC/TUS0127692A

GENERAL INFORMATION:
APPLICANT: BOARD of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
TITLE OF INVENTION NUMBER: PCT/US01/27692A

CURRENT APPLICATION NUMBER: PCT/US01/27692A

CURRENT FILING DATE: 2001-09-07

NUMBER OF SEQ ID NOS: 251

SOFTWARE: PatentIn version 3.1
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US-10-784-537-3
                               US-LU-/84-53/-3

Sequence 3. Application US/10784537

GENERAL INFORMATION:
APPLICANT: ARAP, WADIH
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: MARCHIO, SEENA
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: ANINOPERTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: ANINOPERTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
FILE REFERENCE: UTSC: 872US
CURRENT APPLICATION NUMBER: US/10/784,537
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
PRIOR PRIOR PRESENTION NUMBER: 60/231,266
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PRIOR PRESENTION NUMBER: 2000-09-08
PRIOR PRIOR DATE: 2010-09-08
PRIOR PRIOR PRIOR DATE: 2010-09-08
PRIOR PRIOR DATE: 2010-09-08
PRIOR PRIOR DATE: 2010-09-08
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Pred. No. 13;
0; Mismatches 1; Indels
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LOCATION: (1)..(31)
CHER INFORMATION: synthetic construct
PCT-USO1-27692A-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserva
                   US-10-784-537-3
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: America only)
TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: and Adipose Tissues
FILE REPERBNCE: 5774.P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
CURRENT PILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENTRAL 1870: Application US/10363204
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
TILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 13
                                                                                                                                                                                                                                       APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
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Pred. No. 2.2;
0; Mismatches
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88.9%; Pred. No. 2.2;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 13
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                               CPRECESNC 13
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APPLICANT:
APPLICANT:
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| Sequence 9, Application US/10784537
| Sequence 9, Application US/10784537
| GENERAL INFORMATION:
| APPLICANT: ARAP, WADIH
| APPLICANT: PASQUALINI
| APPLICANT: LAHDENRANTA, JOHANNA
| TITLE OF INVENTION: AMINOPERPTIDASE A (APA) TARGETING PEPTIDES
| TITLE OF INVENTION: AMINOPERPTIDASE A (APA) TARGETING PEPTIDES
| TITLE OF INVENTION: AMINOPERPTIDASE A (APA)
| TITLE OF INVENTION: AMINOPERPTIDASE A (APA)
| CURRENT PELING DATE: 2004-02-23
| PRIOR APPLICATION NUMBER: PCT/US01/27692
| PRIOR APPLICATION NUMBER: PCT/US01/27692
| PRIOR PILING DATE: 2001-09-07
| PRIOR PILING DATE: 2001-09-07
| PRIOR PILING DATE: 2001-09-07
| PRIOR APPLICATION NUMBER: 09/765,101
| PRIOR PILING DATE: 2000-09-08
| PRIOR APPLICATION NUMBER: 60/231,266
| PRIOR APPLICATION NUMBER: 60/231,266
| PRIOR APPLICATION NUMBER: 60/231,266
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 13
| SEQ ID NO 9
| LENGTH: 31
| LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-784-537-1
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APPLICANT: MARCHIO, SERENA
APPLICANT: LAHDENRANTA, JOHANNA
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
FILE REPERENCE: UTSC:872US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.5%; Score 47; DB 33; Length 31; 88.9%; Pred. No. 13;
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                                                                                                                                                  CURRENT FILING DATE: 2004-02-23
CURRENT FILING DATE: 2004-02-23
PRIOR PELLING DATE: 2004-02-23
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FLING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
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PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.5.
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TITLE OF INVENTION: Compositions and Methods of Use of Targeting Peptides Against Pla
TITLE OF INVENTION: Compositions and Adipose Tissues
FILE REFERENCE: 5774.P009PCT
CURRENT APPLICATION NUMBER: PCT/US02/27836
CURRENT APPLICATION NUMBER: PCT/US01/27692
PRIOR APPLICATION NUMBER: PCT/US01/27692
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
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GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INFORMIN: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REPERENCE: 005774, P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
                                                                                               APPLICANT: Board of Regents, The University of Texas System (applicant for the APPLICANT: purposes of all designated states except US)
APPLICANT: Pasqualini, Renata (applicant for the purpose of the United States of APPLICANT: America only)
APPLICANT: Arap, Wadih (applicant for the purpose of the United States of America
                                                                                                                                                                                                                                                                    APPLICANT: Kolonin, Mikhail G. (applicant for the purpose of the United States of APPLICANT: America only)
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82.5%; Score 47; DB 1; Length 31;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Peptide PCT-US02-27836-58
                                            Application PC/TUS0227836
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; Sequence 1, Application US/10784537
; SEMERAL INFORMATION:
; APPLICANT: ARAP, WADIH
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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APPLICANT: MASCUALINI
APPLICANT: MASCUALINI
APPLICANT: MASCUALINI
APPLICANT: MARCHIO, SERENA
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION: FOR THE TREATMENT OF CANCER
TITLE OF INVENTION NUMBER: BCT/USO1/27692
PRIOR PELLING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
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APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: PASQUALINI
APPLICANT: MARCHIO, SERBNA
TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TRRATMENT OF CANCER
TITLE OF INVENTION: POR THE TRRATMENT OF CANCER
FILE REFRENCE: UTSC: 972US
CURRENT APPLICATION NUMBER: US/10/784,537
CURRENT APPLICATION NUMBER: PCT/US02/27836
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,266
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-08
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
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                            1; Indels
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                      RESULT 14
US-10-784-537-5
Sequence 5, Application US/10784537
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10784537
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                    CIRECESIC 13
                                                                                    CPRECESIC 9
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## PRIOR FILING DATE: 2000-09-08

| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 6
| LENGTH: 8
| TYPE: PRT
| ORGANISM: Artificial Sequence
| FEATURE:
| OTHER INFORMATION: Description of Artificial Sequence: Synthetic
| OTHER INFORMATION: Peptide
| OTHER INFORMATION: Peptide
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Sequence 60, Application US/10489071

GENERAL INFORMATION:
APPLICANT:
 WIMBER:
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AND ANIPOSE TISSUES
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER:
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Best Local Similarity 100.0%; Pred. No. 7.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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             1 CPRECESIC 9
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US-10-489-071-60
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Sequence 50, Appl
Sequence 18045, Appl
Sequence 26731, A
Sequence 6, Appl
Sequence 23, Appl
Sequence 57, Appl
Sequence 79, Appl
Sequence 79, Appl
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                                                                                                      November 16, 2004, 14:24:42; Search time 4.07547 Seconds (without alignments) 40.083 Million cell updates/sec
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Sequence 222:
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1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2 6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2 6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2 6/ptodata/1/paa/US08_NEW_COMB.pep:*

6: /cgn2 6/ptodata/1/paa/US08_NEW_COMB.pep:*

7: /cgn2 6/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /cgn2 6/ptodata/1/paa/US11_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                         80665 seqs, 18150633 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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57
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Match Length
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Perfect score:
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Gaps

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RESULT 1

US-10-489-071-56

US-10-489-071-56

SEQUENCE 56, Application US/10489071

SEQUENCE 56, Application US/10489071

SEQUENCE 56, Application US/10489071

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USB OF TARGETING PEPTIDES AGAINST

TITLE OF INVENTION: PACCHATA AND ADIPOSE TISSUES

TITLE OF INVENTION: PACCHATA AND ADIPOSE TISSUES

TITLE OF INVENTION: PACCHATA AND ADIPOSE TISSUES

CURRENT FILING DATE: 2004-03-08

PRIOR FILING DATE: 2002-08-30

NUMBER OF SEQ ID NOS: 144

SEQ ID NO 56

LENGTH: 9
                            Sequence 14220, A
Sequence 14220, A
Sequence 14222, A
Sequence 14185, A
Sequence 14113, A
Sequence 14219, A
Sequence 19, Appl
Sequence 19, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 165, Appl
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
Sequence 1654, A
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Sequence 1
Sequence 1
                   US-10-732-923-14187

US-10-732-923-14187

US-10-732-923-14220

US-10-732-923-14222

US-10-732-923-14223

US-10-732-923-14213

US-10-732-923-14213

US-10-732-923-14219

US-10-732-923-14219

US-10-970-192-192

US-10-970-192-192

US-10-732-923-3520

US-10-732-923-3520

US-10-732-923-3520

US-10-220-366A-14624

US-10-220-366A-14624

US-10-220-366A-14624

US-10-733-923-923-195
                                                                                                                                                                                                                      US-10-735-256-4
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Gaps
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GENERAL INFORMATION:
APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: CUSTOM
SEQ ID NO 26731
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 6; Length 388;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORCANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (388)
CTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-26731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234B
FILLING DATE: 19-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/828683
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09993234B GENERAL INFORMATION:
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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                      CPRECESIC
                                                                                                                                             US-10-220-366A-26731
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US-09-993-234B-6
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US-10-489-071-58
US-10-489-071-58
Sequence 59, Application US/10489071
GENERAL INFORMATION:
APPLICANT: PASQUALINE TAL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST;
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILE REPRENCE: UTSC:8560S
CURRENT PILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: PCT/US02/27836
PRIOR PILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PATENTIN VERSION 3.1
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; Sequence 18045, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides
; FILE REPERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR PILING DATE: 2000-05-18
; PRIOR PILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: CUSTOM
; SEQ ID NO 18045
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 6; Length 31; Pred. No. 0.15;
                                                                                                    Score 50; DB 6; Length 13;
Pred. No. 0.024;
0; Mismatches 1; Indels
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; OTHER INFORMATION: Xaa = any amino acid or nothing US-10-220-366A-18045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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                                     ; OTHER INFORMATION: Synthetic Peptide US-10-489-071-60
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                                                                                                    87.78;
88.98;
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55.6%;
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 31
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-765-727-23
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US-10-976-102-78
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APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: YOUNG, LESIEY LYNN
TITLE OF INVENTION: WODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
FILE REFERENCE: 674525-2010
CURRENT APPLICATION NUMBER: 2004-01-23
PRIOR PELICATION NUMBER: PCT/GB02/03426
PRIOR PELICATION NUMBER: PCT/GB02/03426
PRIOR PELICATION NUMBER: GB 0118153.6
PRIOR PELICATION NUMBER: GB 0212282.8
PRIOR PELICATION NUMBER: GB 0212282.8
PRIOR PELICATION NUMBER: GB 0212283.6
PRIOR PELICATION NUMBER: GB 0212283.6
PRIOR PELICATION NUMBER: GB 0212283.6
PRIOR PELICATION NUMBER: GB 0212283.6
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-38
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATCENTIN VET: 3.2
SEQ ID NO 23
LENGTH: 2471
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US-10-411-910B-48

Sequence 48, Application US/10411910B

GENERAL INFORMATION:

APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes

FILE REFERENCE: H2041203-P

CURRENT APPLICATION NOTE: 2003-04-12

NUMBER OF SEQ ID NOS: 363

SEQ ID NO 48

LENGTH: 844
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                                                                                                                                                                                                                                                                                              Query Match 64.9%; Score 37; DB 5; Length 417; Best Local Similarity 44.4%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                      3; Indels
REFERENCE/DOCKET NUMBER: P1007P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ; ORGANISM: Desulfitobacterium hafniense US-10-411-910B-48
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64.9%; Score 37; DB 6; Length 2471; 75.0%; Pred. No. 2.8e+02; ive 1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT FILING DATE: 2004-10-27
PRIOR PELING DATE: 2001-09-11
PRIOR PILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 106
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j Sequence 57, Application US/10846989

g GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMANUBLE CYRILLE PASCAL
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: TUGAL, TAWARA
APPLICANT: TUGAL, TAWARA
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 65452-2012
CURRENT APPLICATION NUMBER: US/10/846,989
CURRENT APPLICATION NUMBER: COT-6-14
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
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ORGANISM: Arabidopsis thaliana
        Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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1371 PRDCESGC 1378
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APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antinicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
GURRENT APPLICATION NUMBER: US/10/976,102
CURRENT APPLICATION NUMBER: 09/950,933
FRIOR APPLICATION NUMBER: 09/950,933
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NOS: 99
LENGTH: 103
                                                                           Sequence 22211, Application US/10220366A

GENERAL INFORMATION:
APPLICANT: HYSEQ, INC.
TITLE OF INVERTION:
FILE REFERENCE: 21272-042
CURRENT APPLICATION WUMBER: US/10/220,366A
CURRENT APPLICATION WUMBER: 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2001-02-33
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: CUSTOM
SEQ ID NO 22211
LENGTH: 64
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature; LOCATION: (1).T.(64); OTHER INFORMATION: Xaa = any amino acid or nothing US-10-220-366A-22211
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; ORGANISM: Arabidopsis thaliana
US-10-976-102-89
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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US-10-220-366A-17365
                                           RESULT 13
US-10-220-366A-22211
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APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT APPLICATION NUMBER: 09/950,933
PRIOR APPLICATION NUMBER: 09/950,933
PRIOR FILING DATE: 2000-09-13
SPRIOR FILING DATE: 2000-09-13
SOFTWARE: PASSED ID NOS: 99
NUMBER OF SEQ ID NOS: 99
SQOIN NO 96
LENGTH: 106
                                                                                                                                                                                                                                                                                                                            APPLICANT: Samons, Carl R.
APPLICANT: Samons, Carl R.
APPLICANT: Samons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 1278B
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT PILING DATE: 2004-10-27
PRIOR APPLICATION NUMBER: 09/950,933
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastESQ for Windows Version 4.0
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                                         Query Match 63.2%; Score 36; DB 6; Length 80; Best Local Similarity 55.6%; Pred. No. 17; Matches 5; Conservative 1; Mismatches 3; Indels
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Pred. No. 17;
1; Mismatches 3; Indels
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US-10-976-102-79
Sequence 79, Application US/10976102
GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-10-976-102-96
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US-10-976-102-79
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Best Local Similarity 55.6
Matches 5, Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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US-10-976-102-78
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3; Indels

APPLICANT: HYSEQ, INC

48 CPSECDRRC 56

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Search completed: November 16, 2004, 14:47:12 Job time : 4.07547 secs

60 CAHDCDNIC 68

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03; Search time 10.1887 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-2 57 1 CPRECESIC 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ŭ		cal	probable glutamate	NADH-glutamate syn	NADH-dependent glu	,	hemocytin - silkwo	23.5K protein - Ma	23.5K protein - Ma	hypothetical prote	histidine rich cal	histidine-rich cal	hypothetical prote	formate dehydrogen	molybdopterin oxid	reductase [importe	hypothetical prote	AcOrf-70 protein -	polyferredoxin - M	protein V - Hendra	glutamate synthase		glutamate synthase			anti-mullerian hor	hypothetical prote	
SUMMARIES	3 ID	2 AE2094	2 T16246	2 S75952				_	-	1 WMBEMA	L WMBEMB		2 A54660	2 A34373	2 T23680	2 AE3407		2 AG2716		_	2 F64416			2 B75024				2 JC4335	970	: н88085
	Length DB										•	358	669	852	372	708				•	• •	•					54	573	859	888
de	Query	82.5	71.9	70.2	70.2	70.2	70.2	70.2	70.2	68.4	68.4	68.4	68.4	68.4	66.7	66.7	66.7	66.7	66.7	65.8	64.9	•	64.9	64.9	64.9	64.9	64.9	64.9	64.9	64.9
	Score	47	41	40	40	40	40	40				39		39	38	38	38	38	38	37.5	37	37	37	37	37	37	37		37	37
	Result No.	-	7	m	4	υ.	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

71.9%; Score 41; DB 2; Length 273;

Query Match

hypothetical prote transcription fact	GASA4 - Arabidopsi gibberellin-regula	cytosolic acyl-CoA probable acyl-coa	hypothetical prote	glutamate synthase	glutamate synthase	glutamate synthase	protein T23J18.22	hypothetical prote	hypothetical prote	hemagglutinin-neur	hemagglutinin-neur	EMP70 protein prec
T19691 I38414	T49958 S60232	C81662 F71502	T32691	G98262	AC3022	AE3514	H86248	T46720	T15574	HNNZ39	A43487	864915
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1353	106 106	159 160	413	484	484	499	522	539	267	575	575	667
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64 64	63	63	63	63	63	63	63	63	6	63	63	63
37	36 36	36 36	36	36	36	36	36	36	36	36	36	36
30 31	33 33	3.4 3.5	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

	RESULT 1 AB2094 hypothetical protein alr2308 [imported] - Nostoc sp. (strain PCC 7120)
	Cjarettes: Mostoc sp. FCC 7120 is a synonym of Anabaena sp. strain PCC 7120 CjDate: H-DEC-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
	R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NNA Dee, B. 2016, 273
	Afrikace: Office Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AB2094
	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-425 - KURS.
•	A/Cross-references: Unifroligation; Garbacocols; Fibribab/400/.i; Fibribation; Garbarion; A/Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr2308
	Query Match 82.5%; Score 47; DB 2; Length 425; Best Local Similarity 77.8%; Pred. No. 5.4; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	Qy 1 CPRECESIC 9
	Db 112 CPRPCEKIC 120
	RESULT 2
	Argotherical protein P35A5.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
	C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T16246 P:Lainhach D
	submitted to the EMBL Data Library, January 1996 A; Description: The sequence of C. elegans cosmid F35A5.
	A; Reference number: 218485 A; Accession: T16246
	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Docidion: 1 272 - 272
	A, Tross.references: ULS.7 CLEA.7 A, Cross.references: UNIPROT:Q20000, EMBL:U46675, NID:g1166613, PID:g1166614, PIDN:AAB5264 A, Experimental source: strain Bristol N2, clone F35A5
	C;Genetics: A;Gene: CESP:F35A5.4 b.Man nosition. V
	A;Map postiton: A A;Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2

Gaps

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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucł ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:099WD0; GB:BA000018; PID:g13700363; PIDN:BAB41661.1; GSPDB:GAA,Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.; Davies, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A66909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9CDD4; GB:AL450380; NID:g13092455; PIDN:CAC29570.1; GSPDB:GR
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R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
Pereber Dyn. 203, 212-222, 1995, A.; Koyama, B.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
A;Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F86916
NADH-dependent glutamate synthase small subunit gltD [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
C;Accession: F86916
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R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori,
submitted to JIPID, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Spēcies: Gallus gallus (chicken)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 04-Apr-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2;
Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2;
Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: gltD
C;Superfamily: Glutamate synthase, small subunit
                                                                                                                                                                                                                                                                                                                                                                         A;Gene: gltD
C;Superfamily: Glutamate synthase, small subunit
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A;Molecule type: mRNA
A;Residues: 1-835 <MAT>
A;Cross-references: DDBJ:D45365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 CPAPCESAC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 CPAPCESAC 114
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-487 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-488 <STO>
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                                                                                                                                                                                                                                                                                hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Decies: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 875952
C;Accession: 87597
C;Accession: 87597
C;Accession: 87597
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:Q9S2Z0; EMBL:AL109849; PIDN:CAB52860.1; GSPDB:GN00070; SCOED A,Experimental source: strain A3(2) C,Genetics: G,Genetics: A,Gene: gltD; SCOEDB:SC3A3.03c C,Superfamily: glutamate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH-glutamate synthase small subunit gltD [imported] - Staphylococcus aureus (strain N3 C;Species: Staphylococcus aureus C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004 C;Accession: B89813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q55456; BMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA1079
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T34868
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
A;Reference number: Z21560
A;Reference number: T34868
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2; Length 395;
Pred. No. 57;
1; Mismatches 3; Indels
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Pred. No. 66;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: S74322; MUID:97061201; PMID:8905231
                                                  ;
                Pred. No. 31;
4; Mismatches
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66.7%;
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ilarity 55.6%;
Conservative
                   44.48;
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                                            4; Conservative
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                                                                                                                                  ||::|::|
146 CPQQCQPVC 154
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Matches 6: Conserv
             Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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A; Status: nucleic ac
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Gaps

Query Match

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23.5K protein - Marek's disease virus (type 1, strains Md5 and GA)
NyAlternate names: UL45h protein
Cispecies: Marek's disease virus
AiNote: host Gallus gallus (chicken)
Cibate: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
Cipacession: B22818 / Q2207
Cipacession: B22818; Virus
Airle: Comparison of the sequence of the secretory glycoprotein A (GA) gene between Md5
Airle: Comparison of the sequence of the secretory glycoprotein A (GA) gene between Md5
Aireference number: A22818; WUID:90142542; PMID:2559540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Marek's disease virus homologue
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A;Residues: 1-358 «WIL»
A;Cross-references: UNIPROT: (21563; EMBL: Z66498; PIDN: CAA91291.1; GSPDB: GN00020; CESP: M15
A;Experimental source: clone M195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein M195.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23802
R;Burton, J.
R;Burton, J.
A;Reference number: Z19801
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-211 <YAN>
A,Residues: 1-211 <YAN>
A,Cross-references: GB:L10283; NID:g388703; PIDN:AAA03152.1; PID:g388710
A,Experimental source: strain GA
C,Superfamily: turkey herpesvirus 23.5K protein
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   Indels
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A; Residues: 1-211 < IRA>
A; Residues: 1-211 < IRA>
A; Experimental source: Strain Md5
A; Tanagida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A; Title: Nucleotide and predicted amino acid sequences of the control of the 
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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   Mismatches
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A;Introns: 90/3; 162/3; 207/3; 270/2
C;Superfamily: gliadin
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55.6%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
   5; Conservative
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162 CPRTCSVVC 170
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                                                                        1 CPRECESIC 9
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       Matches
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C;Species: Bombyx mori (silkworm)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 12-Jul-2004
C;Accession: 552093; S70920
R;Kotani, B; Yamakawa, M.; Iwamoto, S.; Tashiro, M.; Mori, H.; Sumida, M.; Matsubara, F
Biochim. Biophys. Acta 1260, 245-258, 1995
A;Title: Cloning and expression of the gene of hemocytin, an insect humoral lectin which
A;Reference number: 852093; MUID:95178544; PMID:7873598
A;Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is stron
A;Reference number: JP0076
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23.5K protein - Marek's disease virus (type 1, strain BC-1)
C;Species: Marek s disease virus
C;Species: Marek s disease virus
A;Note: host Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
C;Dates 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
C;Accession: JS0389
R;Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.
Virus Genes 3, 127-140, 1989
A;Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between
A;Reference number: A22818; MUID:90142542; PMID:2559540
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                                                                    A;Accession: JP0076
A;Molecule type: mRNA
A;Residues: 1-835 <MA2>
A;Residues: 1-835 <MA2>
A;Cross-references: DDBJ:D45365
A;Experimental source: 9-6ay embryo
F;273-333/Domain: von Willebrand factor type C repeat homology <VWC>
F;444-80/Domain: EGF homology <EGF1>
F;446-521/Domain: EGF homology <EGF>
F;486-521/Domain: EGF homology <EGF>
F;525-552/Domain: EGF homology <EGF>
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A;Residues: 1-1566,'S',1568-3133 <MOR>
A;Cross-references: EMBL:D29738; NID:g474967; PID:g664884
C;Superfamily: hemolectin/hemocytin
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51;
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A;Residues: 1-3133 <KOT>
A;Cross-references: UNIPROT:P98092; EMBL:D29738
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A;Residues: 1-211 <IHA>
C;Superfamily: turkey herpesvirus 23.5K protein
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submitted to the EMBL Data Library, April 1994
A;Reference number: S70920
A;Accession: S70920
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Pred. No.
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55.6%;
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Matches 5; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity
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Search completed: November 16, 2004, 14:30:51
Job time : 11.1887 secs
                                                                                     Query Match 66.7
Best Local Similarity 55.6
Matches 5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                             184 CPTÉCQPAC 192
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A;Accession: T21680
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-372 <WILD
A;Cross-references: UNIPROT:O17969; EMBL:Z81573; PIDN:CAB04624.1; GSPDB:GN00020; CESP:MC
A;Experimental source: clone M02C9
C;Genetics:
                                                                                                 C;Accession: A54660
R;Hofmann, S.L.; Topham, M.; Haieh, C.L.; Francke, U.
Genomics 9, 656-669, 1991
A;Title: CDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and lc
A;Reference number: A54660; MUID:91244309; PMID:2037293
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A;Molecule type: mRNA
A;Residues: 1-852 <HOF-
A;Cross-references: UNIPROT:P16230; GB:J05080; NID:g165099; PIDN:AAA31279.1; PID:g165100
C;Keywords: calcium binding
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A,Molecule type: mRNA
A,Redidues: 1-699 (ADP)
A,Cross-references: UNIPROT:P23327, GB:M60052, NID:g183918; PIDN:AAA88071.1; PID:g183919
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T23680
R;Matthews, L.
                                                Gaps
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histidine rich calcium binding protein - human
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A;Cross-references: GDB:126369; OMIM:142705
A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
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Best Local Similarity 55.00,
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818 CPLVCETVC 826
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Matches 5; Conserv
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RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 antracellular pathogen Brucella melitensi A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-708 <KUR>
A;Cross-references: UNIPROT:Q8YGB6; GB:AE008917; PIDN:AAL52424.1; PID:g17983227; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                        formate dehydrogenase (EC 1.2.1.2) [imported] - Brucella melitensis (strain 16M)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                     Length 372;
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                                                                                                                  Score 38; DB 2; Length 372
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
A;Map position: 2
A;Introns: 17/3; 72/3; 181/3; 232/2; 258/3; 294/3; 336/1
C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 38; DB 2; I
55.6%; Pred. No. 1.7e+02;
tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: I
C;Superfamily: formate dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                        66.7%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 16M
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model protein search, using ı OM protein November 16, 2004, 14:09:48; Search time 176.642 Seconds (without alignments) 62.956 Million cell updates/sec Run on:

US-10-784-537-1 Title: Perfect score:

1 CYNLCIRECESICGADGACWTWCADGCSRSC 31 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters:

2002273 segs, 358729299 residues

Searched:

seq length: 0 seq length: 200000000 88 Minimum

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04:\* L: geneseqp1980s:\* ٠. Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2004s:\* geneseqp2000s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Abg60450 Selective	Abr56862 Aminopept	Adp31258 Human sec	Adp31260 Human sec	Adp31259 Human sec	Adp31058 Human sec		Adp30638 Human sec	Adp30636 Human sec		Adp30720 Human sec	Adp30699 Human sec	Adp30701 Human sec	Adp30712 Human sec	Adp30722 Human sec	Adp30565 Human sec	σ,	Abj38280 pAMG21-RA	Adp30630 Human sec	Adp30633 Human sec	Adp30606 Human sec	Adp30910 Human sec	Adp30911 Human sec	Adp30681 Human sec	Adp31356 Human sec
SUPERMETES	ΩI	ABG60450	ABR56862	ADP31258	ADP31260	ADP31259	ADP31058	ADP30639	ADP30638	ADP30636	ADP30692	ADP30720	ADP30699	ADP30701	ADP30712	ADP30722	ADP30565	ADP30749	ABJ38280	ADP30630	ADP30633	ADP30606	ADP30910	ADP30911	ADP30681	ADP31356
	DB 1	R	9	œ ~	8	80	8	œ	<b>6</b> 0	00	80	8	80	80	80	80	œ ~	60	9	80	_	80	80	80	œ _	æ
	Query Match Length	31	31	2808	4683	4848	2027	291	291	291	629	629	659	623	659	659	1478	2803	7285	291	291	375	2700	2700	2827	1001
de	Query Match	100.0	100.0	36.9	36.9	36.9	36.1	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.6	35.4	35.4	35.4	35.1	35.1	34.8	34.3
	Score	198	198	73	73	73	71.5	71	71	71	71	71	71	71	71	71	71	71	70.5	70	70	70	69.5	69.5	69	99
	Result No.	7	7	e	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adp30560 Human sec Abr55376 A polypep Ad123896 Buthoid s Adp31445 Human sec		Human Human Human		Human Human Drosop Drosop
ADP30560 ABR55376 ADL23896 ADP31445	ADP31215 ADP30869 ADP31690 ADP30949	ADP31323 ADP31478 ADP31550	ADP31594 ADP31595 ADP31117	ADP31210 ADP31211 ABB71150 ABB58064
<b>∞</b> • • • •				00044
2124 61 61 585	711 507 2358 930	423 1044 1044	2542 3036 3585	1227 1344 2858 3060
33.8	333.8	3223	, w w w w	22222 22222 22222 22222 2222 2222 2222 2222
68 67 67	66.5	65.5	0 0 0 0	64.5 64.5 64.5 64.5 64.5 64.5 64.5 64.5
25 28 28 38 38 38	333	9 8 8 9 6 9 6 9 6 9 6 9 6 9 6 9 9 9 9 9	7 8 8 8 7 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1 4 4 4 4 1 6 6 4 6

### ALIGNMENTS

ABG60450 standard; peptide; 31 AA ABG60450

ABG60450;

(first entry) 30-JUL-2002

Selective targeting peptide #125.

Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammation; macular degeneration; entinflammatory; antidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic; gene therapy 

Synthetic.

WO200220769-A1.

14-MAR-2002.

07-SEP-2001; 2001WO-US027692.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R; Arap W,

WPI; 2002-415731/44.

Targeting peptides identified by phage display, useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular disease.

Claim 22; Page 108; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

Gaps

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Length 31; Indels

100.0%; Score 198; DB 6; 100.0%; Pred. No. 8.6e-14; iive 0; Mismatches 0;

Conservative

31 31

888888888

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1 CYNLCIRECESICGADGACWTWCADGCSRSC
                                                                                                                     CYNLCIRECESICGADGACWTWCADGCSRSC
                      Similarity
31; Conser
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      Query Match
                          Local
                        Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for treating obesity or a selective for adipose tissue; (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and dipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immundeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teraregenic activity. ABRS6806 to ABRS6827 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention
inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABGG0326-ABGG0574 represent selective targeting peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to
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                                                                                                                                                                                   Length 31;
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                                                                                                                                                                                 100.0%; Score 198; DB 5;
100.0%; Pred. No. 8.6e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  CYNLCIRECESICGADGACWTWCADGCSRSC 31
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                                                                                                                                                                                                                                                                                                                                                                                                      ABR56862 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002; 2002WO-US027836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasqualini R, Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-371749/35.
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003022991-A2
                                                                                                                                            Sequence 31 AA;
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                                                                                                                                                                                                      Best Local Sim.
Matches 31;
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                             Human secreted protein SEQ ID #2025
ADP31258 standard; protein; 2808
                                                                                                                                                                                                                                                                                                       2002US-0410958P.
2002US-0410959P.
2002US-0410960P.
2002US-0410961P.
2002US-0410961P.
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2002US-0410949P.
2002US-0410953P.
2002US-0410957P.
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2002US-0411023P.
2002US-0411024P.
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                                                                                                                                 28-AUG-2003; 2003WO-US026780.
                                                                                                                                                                                                                                            002US-0406655P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0411111P
2003US-0463700P
                              (first entry)
                                                                                                  WO2004035732-A2.
                                                                                                                                                                                             29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                         17-SEP-2002;
17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                        17-SEP-2002;
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29-AUG-2002;
                              12-AUG-2004
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Sequence 31 AA;

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2002US-0411046P.
2002US-0411048P.
2002US-0411052P.
2002US-0411055P.
                                                                                                                      2002US-0406608P.
2002US-0406611P.
2002US-0406612P.
2002US-0406612P.
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2002US-0406642P.
2002US-0406646P.
2002US-0406653P.
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2002US-0406666P.
2002US-0410946P.
2002US-0410947P.
2002US-0410948P.
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2002US-0411082P.
2002US-0411101P.
2002US-0411111P.
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2003US-0463708P.
2003US-0463716P.
2003US-0463732P.
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2003US-0467201P.
2003US-0467203P.
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                   WO2004035732-A2.
Homo sapiens.
                                                                                                                                                                                                                                                                                                               17-SEP-2002;
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                                       29-APR-2004
83
                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antichinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule for diagnosing, preventing or treating diss
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                         Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.9%; Score 73; DB 8; Length 2808; 45.2%; Pred. No. 42; tive 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1974 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3256; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein SEQ ID #2027.
                                                                                                                                                                                                                                                                      (FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP31260 standard; protein; 4683 AA
                  2003US-0463732P.
2003US-046719P.
2003US-0467201P.
2003US-0467201P.
2003US-0467230P.
2003US-0471336P.
                                                                                                                                2003US-0485218P.
2003US-0485223P.
2003US-0485224P.
2003US-0485325P.
                                                                                        2003US-0472420P.
2003US-0472430P.
2003US-0476609P.
2003US-0476641P.
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2003US-0493370P.
2003US-0493573P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                  18-APR-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
09-JUN-2003; 2
                                                                                                                                                                                                                                                                                         Williams LT,
Halenbeck RF,
                                                                                                                                                                08-JUL-2003;
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Matches
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and
                                                                                                                                                  17-SEP-2002;
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19-MAY-2003;
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22-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                     02-MAY-2003;
                                                                                                                                                                                                               17-SEP-2002;
  1;
                                                                                                                        New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                                                                                       The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antibidiammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                              Hestir K, Beaurang PA, Behrens D;
hakota S, Haishan L, Linnemann T;
                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                          Match 36.9%; Score 73; DB 8; Length 4683; Local Similarity 45.2%; Pred. No. 65; es 14; Conservative 1; Mismatches 14; Indels
                                                                                   Zhang H;
                                                                                                                                                                                                                                                                                                                                                                 2049 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2077
                                                                                                                                                                                                                                                                                                                                                   1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                                                    Claim 1; SEQ ID NO 3258; 428pp; English.
                                                            Williams LT, Chu K, Lee E, Hestir K,
Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein SEQ ID #2026.
                                                                                                                                                                                                                                                                                                                                                                                                                            ADP31259 standard; protein; 4848 AA
                                          (FIVE-) FIVE PRIME THERAPEUTICS INC
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2002US-0406588P.
2002US-040661BP.
2002US-0406612P.
2002US-0406612P.
2002US-0406616P.
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2002US-0406655P.
08-AUG-2003; 2003US-0493370P.
08-AUG-2003; 2003US-0493573P.
08-AUG-2003; 2003US-0493577P.
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2002US-0406579P
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                                                                                                       WPI; 2004-348438/32.
                                                                                                                                                                                                                                                                                       Sequence 4683 AA;
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29-AUG-2002;
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29-AUG-2002;
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New nucleic acid molecule for diagnosing, preventing or treating dise such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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2002US-0411023P.
2002US-0411024P.
                                           2002US-0411032P.
2002US-0411035P.
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2002US-0411041P.
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2003US-0471306P.
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diseases

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02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
09-JUN-2003; 2
09-JUN-2003; 2
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02-MAY-2003;
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Matches
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treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWRB and is not in the specification.
                                                                  Gaps
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                                                  Score 73; DB 8; Length 4848;
Pred. No. 67;
1; Mismatches 14; Indels
                                                                                        2214 CTTTCTGTCCCACGAGGACCTGC--GCTTCC 2242
                                                                                CYNLCIRECESICGADGACWTWCADGCSRSC 31
                                                                                                                                   ADP31058 standard; protein; 2027 AA
                                                                                                                                                                             Human secreted protein SEQ ID #1825
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2002US-040668P.
2002US-040661P.
2002US-0406612P.
2002US-0406612P.
2002US-0406640P.
2002US-0406646P.
2002US-0406646P.
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2002US-0406653P.
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2002US-0410960P.
2002US-0410961P.
2002US-0411019P.
2002US-0411022P.
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2002US-0410946P.
2002US-0410947P.
2002US-0410948P.
                                                   36.9%;
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                                                                                                                                                               (first entry)
                                                                  Conservative
                                                         Local Similarity
                                     Sequence 4848 AA;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
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29-AUG-2002;
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                                                  Query Match
                                                                                                                                                 ADP31058
                                                            Best Loc
Matches
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diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chu K, Lee E, Hestir K, Beaurang PA, Behrens D, Huang MM, Kothakota S, Haishan L, Linnemann T; ang Y, Wong JGP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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2003US-0472430P
2003US-0476609P
2003US-0486218P
2003US-0485218P
2003US-0485224P
2003US-0485225P
2003US-0485225P
2002US-0411055P.
2002US-0411073P.
2002US-0411101P.
2002US-0411111P.
2003US-0463700P.
2003US-0463700P.
2003US-0463716P.
2003US-0467199P.
2003US-0467201P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                               K, Beaurang PA, Behrens D
, Haishan L, Linnemann T;
Zhang H;
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                                                                                                                                                                                Hestir K,
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2637; 428pp; English
                                                                                                                                                                                Williams LT, Chu K, Lee E, Hestir K.
Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G,
                                                                                                                                                       (FIVE-) FIVE PRIME THERAPEUTICS INC.
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2002US-0406585P.
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29-AUG-2002; 2002US-0406579P.
29-AUG-2002; 2002US-0406585P.
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
                                                      15-JUL-2003; 2
15-JUL-2003; 2
08-AUG-2003; 2
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08-AUG-2003;
08-AUG-2003;
 08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
14-JUL-2003;
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Matches
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                                                       Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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2003US-0463716P.
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2003US-0467199P.
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2002US-0411111P.
2003US-0463700P.
                             Human secreted protein SEQ ID
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2002US-0406608P.
2002US-0406611P.
2002US-0406612P.
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2002US-0410949P.
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2002US-0411055P.
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(first entry)
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18-APR-2003;
02-MAY-2003;
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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02-MAY-2003;
                                                                                                 Homo sapiens
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29-AUG-2002;
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18-APR-2003;
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19-MAY-2003;
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17-SEP-2002;

17-SEP-2002;

17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 17-SEP-2002; 7-SEP-2002; 7-SEP-2002; 7-SEP-2002;

7-SEP-2002

17-SEP-2

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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                 The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immunos, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                      8; Length 291;
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                                                                                                                                                                                      Score 71; DB 8
Pred. No. 9.6;
2; Mismatches
           Claim 1; SEQ ID NO 2636; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein SEQ ID #1403
                                                                                                                                                                                                                                                                                                                                           ADP30636 standard; protein; 291 AA
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2002US-0406588P.
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2002US-0410947P.
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57.9%;
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                                                                                                                                                                                                    Local Similarity 57.9 es 11; Conservative
                                                                                                                                                              Sequence 291 AA
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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Best Local Si
Matches 11;
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L, Linnemann T;
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Halenbeck RF, Huang MM, Kothakota S, Haishan L,
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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2003US-0463700P
2003US-0463716P
2003US-0463732P
2003US-046719P
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2003US-0467203P
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2003US-0486960P.
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2002US-0406653P.
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02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
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22-MAY-2003;
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9-MAY-2003;

08-AUG-2003

.7-SEP-2002

8-APR-2003

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17-SEP-2002;

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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                        Human secreted protein SEQ ID #1459.
                          ADP30692 standard; protein; 659 AA.
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2002US-0411023P
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2002US-0411019P.
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2003US-0471306P
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
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RESULT 10
            ADP30692
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thakota S, Haishan L, L.
Wu G, Zhang H;
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                      2002US-0411041P
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2003US-0493370P.
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02-MAY-2003;
02-MAY-2003;
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18-APR-2003;
18-APR-2003;
02-MAY-2003;
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19-MAY-2003;
22-MAY-2003;
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09-JUN-2003;
09-JUN-2003;
08-JUL-2003;
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Pierce K, Wa
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Query Match Best Loca Matches

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Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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Halenbeck RF, Huang MM, Kothakota S,
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            2002US-0406579P.
2002US-040658PP.
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such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.
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Haishan L, Linnemann T;
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                                                                                                                                                                                                                            Chu K, Lee E, Hestir K,
Huang MM, Kothakota S, 1
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                                                                                                                                                                                                       (FIVE-) FIVE PRIME THERAPEUTICS INC
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19-MAY-2003; 2003US-0471336P.
22-MAY-2003; 2003US-0472420P.
22-MAY-2003; 2003US-0472430P.
09-JUN-2003; 2003US-047669P.
09-JUN-2003; 2003US-0476641P.
08-JUL-2003; 2003US-0485218P.
08-JUL-2003; 2003US-0485224P.
08-JUL-2003; 2003US-048632P.
14-JUL-2003; 2003US-0486480P.
15-JUL-2003; 2003US-0486480P.
15-JUL-2003; 2003US-0486480P.
15-JUL-2003; 2003US-0486480P.
15-JUL-2003; 2003US-0486891P.
15-JUL-2003; 2003US-048690P.
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                                                                                                                                    2003US-0486960P.
2003US-0493341P.
2003US-0493370P.
2003US-0493573P.
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les 11; Conservative
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Matches
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ADP30720
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, anticharmatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2697; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 659 AA;
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                                                                        New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                    The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antihilammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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    Zhang H;
                                                                                                                                                               Claim 1; SEQ ID NO 2718; 428pp; English
  Wu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein SEQ ID #1466.
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2002US-0406611P.
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2002US-0406642P.
2002US-0406646P.
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2002US-0410946P.
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                                          WPI; 2004-348438/32.
Pierce K, Wang Y,
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Haishan L, Linnemann T;
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Halenbeck RF, Huang MM, Kothakota S, Haisha
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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17-SEP-2002;
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8; Length 659;

35.9%; Score 71;

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2003US-0467203P.
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Best Local Similarity
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18-APR-2003; 2
18-APR-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
09-JUN-2003; 2
09-JUN-2003; 2
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08-JUL-2003; 2
08-JUL-2003; 2
14-JUL-2003; 2
14-JUL-2003; 2
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                                                                                                                                                         Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
          Gaps
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         9
 ed. No. 19;
Mismatches
57.9%; Pred. No.
                                                                                                                                         Human secreted protein SEQ ID #1468.
                                                                                     ADP30701 standard; protein; 659 AA
                          CGADGACWTWCADGCSRSC 31
                                    35 CGAGGCCTGCAGGCTTTC 53
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2002US-0406585P.
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Best Local Similarity 57.9
Matches 11; Conservative
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                                                                                                                                                                                                                    New nucleic acid molecule for diagnosing, preventing or treating disesuch as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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       PA, Benram. T;
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Williams LT, Chu K, Lee B, Hestir K, Beaurang PA
Halenbeck RF, Huang MM, Kothakota S, Haishan L,
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                   The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immunos, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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Haishan L, Linnemann T;
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                                                                Williams LT, Chu K, Lee B, Hestir K,
Halenbeck RF, Huang MM, Kothakota S, 1
Pierce K, Wang Y, Wong JGP, Wu G, Zh
                                                                                                                                                                                                            Claim 1; SEQ ID NO 2710; 428pp; English
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                                        (FIVE-) FIVE PRIME THERAPEUTICS INC.
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Matches 11; Conserv
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## (FIVE-) FIVE PRIME THERAPEUTICS INC.

Beaurang PA, Behrens D; Haishan L, Linnemann T; Zhang Williams LT, Chu K, Lee E, Hestir K, Halenbeck RF, Huang MM, Kothakota S, 1 Pierce K, Wang Y, Wong JGP, Wu G, Zh, Williams LT, Halenbeck RF,

### WPI; 2004-348438/32

New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.

# Claim 1; SEQ ID NO 2720; 428pp; English.

The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antifinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory,

ö immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification. Gaps ; 8; Length 659; 6; Indels / Match 35.9%; Score 71; DB Local Similarity 57.9%; Pred. No. 19; nes 11; Conservative 2; Mismatches completed: November 16, 2004, 14:24:18 13 CGADGACWIWCADGCSRSC 31 caagecerrecagerrre 53 time : 178.642 secs Sequence 659 AA; Query Match Best Local Si Matches 11; 35 Search Job tim 888888 ઠે 셤

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Best Local Similarity 50.0
Matches 10; Conservative
TOPOLOGY: linear;
MOLECULE TYPE: peptide
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US-08-451-472-6
\begin{array}{c} \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{v} & \mathbf{v} \\ \mathbf{
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Sequence 25, Appli
Sequence 3, Appli
Sequence 3845, A
Sequence 3845, A
Sequence 3845, A
Sequence 14, Appli
Sequence 17, Appli
Sequence 27, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 26, Appli
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                                                                                                                                                                                                                                  November 16, 2004, 14:16:01; Search time 43.8679 Seconds (without alignments) 46.865 Million cell updates/sec
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Sequence 2235
Sequence 13,
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-933-314-24
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US-08-92-70-767-38435
US-09-270-767-38435
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US-09-270-767-38435
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US-08-953-384-1
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Minimum DB Maximum DB

Database

Result Š. Searched:

Sequence:

Run on:

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Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 19249, A
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 48539, A
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US-UB-451-472-6

Sequence 6. Application US/08451472

Patent No. 57701922

GENERAL INFORMATION:

PAPLICANT:
TITLE OF INVENTION: BIOLOGICAL CONTROL ACENTS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: 73
CORRESPONDENCE ADDRESS: 73
CONTRY: USA

STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 18th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STREET: 8th Floor
COMPUTER: 18th Floor
STREET: 18th Floor
COMPUTER: 18th Floor
COMPUTER: 18th Floor
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US-08-820-970-9
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US-09-132-652-2
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REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REPRENENCE JOCKET NUMBER: 117-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816 4100
TELEFAX: (703) 816 4100
                                                         CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,125
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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55.6%;
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Best Local Similarity 55.57
Best Local Similarity
Conservative
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; MOLECULE TYPE: peptide
US-08-451-472-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                             APPLICANT: ATKINSON, RONALD K
APPLICANT: ATKINSON, MERLIN E.H.
APPLICANT: TYLER, MAGGARET I
APPLICANT: TVLER, PURKEY, BUWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.8%; Score 67; DB 1; Length 61; 55.6%; Pred. No. 1.9;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/682,485

FILING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933

FILING DATE: 29-JULY-1994

APPLICATION NUMBER: W0 93/15108

FILING DATE: 29-JULY-1992

APPLICATION NUMBER: AU PL0722

FILING DATE: 31-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 38,301

REGISTRATION NUMBER: 38,301

REGISTRATION INFORMATION:

TELEPHONE: 510-231-1122

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           Sequence 25, Application US/08682485A Patent No. 5763568 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           3: Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08451472; Patent No. 5770192
GENERAL INFORMATION:
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Richmond
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
XX: linear
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ORGANISM: Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94804
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US-08-451-472-4
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| Sequence 25, Application US/0893314
| Sequence 25, Application US/0893314
| Sequence 25, Application US/0893314
| Sequence 25, Application US/0893314
| Settle No. 5959482
| APPLICANT: APPLICANT: TYLER, MARGARET I
| APPLICANT: VONARX, EDWARD I
| TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
| NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS: ADDRESSE: Zeneca, Inc. | STREET: 1200 South 47th Street
| CITY: Richmond | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: California | STATE: Califor
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Pred. No. 1.9;
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TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
WINDER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,472 FILING DATE:
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Sequence 53652, Application US/09270767

Sequence 53652, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7236-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 53652

LENGTH: 79
                                                                                                          US-09-270-767-38435

Sequence 38435, Application US/09270767

Sequence 38435, Application US/09270767

Sequence 38435, Application US/09270767

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 38435

LENGTH: 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 67; DB 4; Length 79; 42.9%; Pred. No. 2.4; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-38435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CESICGADG-----ACWIWCADGCSRSC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 CQSXCSGHGGNRHSSCWSRCGNGC-RSC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 COSXCSGHGGNRHSSCWSRCGNGC-RSC 60
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-472-053-2; Sequence 2, Application US/08472053; Patent No. 6689356; GENERAL INFORMATION:
21 CNKECKSYGGSYGYCWTW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ZLOTKIN, ELLAHU
APPLICANT: MAEDA, SUSUMU
APPLICANT: MCCUTCHEN, BILLY F.
APPLICANT: HAMMOCK, BRUCE D.
APPLICANT: FOWLER, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-270-767-53652
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: MAEDA, SUSUMU
APPLICANT: MCCUTCHEN, BILLY F.
APPLICANT: MCCUTCHEN, BILLY F.
APPLICANT: HAWOCK, BRUCE D.
APPLICANT: HOWLER, ELIZABETH
APPLICANT: BELGABLE, RAMA M.
TITLE OF INVENTION: RECOMBINAN M.
TITLE OF INVENTION: RECOMBINAN M.
TITLE OF INVENTION: LOSS 1.FWCF2
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 07/22603
PRIOR PILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASLEQ FOR WINGON VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%; Score 67; DB 4; Length 61; 55.6%; Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE: ORGANISM: Leiurus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Leiurus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 2;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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                                                                                                                                                                                                                                                                                        REFERENCE DOCKET WINDER: 20,301
REFERENCE DOCKET WINDER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1112
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-UDL-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAMB: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08472053
; Patent No. 6689356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 CNKECKSYGGSYGYCWTW 38
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 55.6*
... 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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LENGTH: 61
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5 CIRECESICGADGACWTW 22

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US-08-952-383A-14
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APPLICANT: ZLOTKIN, ELIAHU
APPLICANT: ZLOTKIN, ELIAHU
APPLICANT: MAEDA, SUSUMU
APPLICANT: MAEDA, SUSUMU
APPLICANT: HAMMOCK, BRUCE D.
APPLICANT: FOWLER, ELIZABETH
APPLICANT: BELAGALE, RAMA M.
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: INSECT TOXINS
FILE REFRERENCE: UCOS8.1FWCP2
CURRENT APPLICATION NUMBER: 08/229417
PRIOR APPLICATION NUMBER: 09/229417
PRIOR FILING DATE: 1994-04.15
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
NUMBER OF SEQ ID NOS: 49
SCOFFWARE: FREELSEQ FOR WINDOWS Version 4.0
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE REPERENCE: UCOSB.1FWCD2
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT PILING DATE: 2002-11-13
PRIOR PILING DATE: 1994-04-15
PRIOR PILING DATE: 1994-04-15
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1990-12-19
PRIOR FILING DATE: 1980-12-19
PRIOR FILING DATE: 1980-12-19
SEQ ID NOS: 49
LUMBER OF SEQ ID NOS: 49
LUMBER OF SEQ ID NOS: 49
LENGTH: 61
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%; Score 64; DB 4; Length 62; 50.0%; Pred. No. 3.9;
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Pred. No. 3.9;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Leiurus quinquestriatus hebraeus
US-08-472-053-2
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US-08-952-383A-14
; Sequence 14, Application US/08952383A
; Patent No. 6096304
; Patent No. Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/08472053 Patent No. 6689356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 CDKECKAYGGSYGYCWTW 38
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.3%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 9; Conservative
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APPLICANT: BILLY F. MCCUTCHEN
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT BACULOVIRUSES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY
TITLE OF INVENTION: RECOMBINANT BACULOVIRUS INSECTICIDES NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 INCH
COMPUTER: IBM
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 3;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IM PC COMPATIBLE
SOFTWARE: MICROSOFT OFFICE 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,264A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                     BA-9063-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,120
FILING DATE: DECEMBER 22, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BEARDELL, LORI Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BA-9078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA-9078
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; Sequence 27, Application US/08970264A
; Patent No. 6322781
                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: BA-90
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CIRECESICGADGACWTW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :||:: |: |||||
40 CDKECKAYGGSYGYCWTW 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.3%;
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TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0°
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Gaps

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APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
TITLE OF INVENTION: Nematode Related Thereto
FILE REPERENCE: 21101.0009U3
FURENT APPLICATION NUMBER: 08/09/627,650B
CURRENT APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR PELING DATE: 1999-11-09
PRIOR PELING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NOS: 50
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Wemthode Neuromuscular Junction GABA Receptors and
FITLE OF INVENTION: Methode Related Thereto
FILE REPERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107727
PRIOR APPLICATION NUMBER: 60/107727
PRIOR PELING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 5:
LENGTH: 1917
                                                                                                                                                                                                                                  Score 61.5; DB 3; Length 5405;
Pred. No. 3.5e+02;
4; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.6%; Score 60.5; DB 4; 40.7%; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | | | | | | | : | 944 CAGTCTATCAAGGTCGT-CAATCATAC 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09627650B; Patent No. 6406872; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-436-063C-5; Sequence 5, Application US/09436063C; Patent No. 6407210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Caenorhabditis elegans
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TELECOMMUNICATION INFORMATION:
                    TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 41.4%;
Matches 12; Conservative
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Best Local Similarity 40.77
Best Local 11; Conservative
                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                               amino acid
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| Patent No. 6271362 |
| GENERAL INFORMATION: APPLICANT: HARADA, MINORU APPLICANT: HARADA, NAOKI |
| TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING TITLE OF SEQUENCES: 29 CORRESPONDENCE 29; CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: STREET: PO BOX 747 CITY: FALLS CHURCH
                                                            Score 64; DB 3; Length 80;
Pred. No. 4.9;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 85;
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ZIP: 22040-0747
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 4
Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
FILE REPERENCE: BB1375 US NA
CURRENT APPLICATION NUMBER: US/09/599,632
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140,410
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SOFTWARE: 85
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NAME: WIRPHY JR., GERALD M
REGISTATION NUMBER: 28,971
REFERENCE/DOCKET NUMBER: 0230-111
                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09599632
Patent No. 6768002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Leiurus quinquestriatus
US-09-599-632-22
                                                                                                                                                 5 CIRECESICGADGACWIW 22
                                                                                                                                                                            40 CDKECKAYGGSYGYCWTW 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.3%;
50.0%;
                                                              Query Match 32.3%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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; MOLECULE TYPE: protein US-08-970-264A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     US-09-599-632-22
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Query Match 30.6%; Score 60.5; DB 4; Length 1917;
Best Local Similarity 40.7%; Pred. No. 1.8e+02;
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps
US-09-436-063C-5
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5 CIRECESICGADGACWTWCADGCSRSC 31
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944 CAGTCTATCAAGGTCGT-CAATCATAC 969 q ð

Search completed: November 16, 2004, 14:32:10 Job time : 44.2013 secs

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greater than or equal to the score of the result being printed,
derived by analysis of the total score distribution.
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75.615 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                              ; Search time 145.057 Seconds
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1: \( \cgn2 \frac{6}{\prodata} \) \( \text{Dubpaa} \) \( \text{USOT} \) \( \text{PUBCOMB} \) \( \text{Dep} : * \)

2: \( \cgn2 \frac{6}{\prodata} \) \( \text{Dubpaa} \) \( \text{USOT} \) \( \text{PUBCOMB} \) \( \text{Dep} : * \)

3: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{NEW} \) \( \text{PUB DEP} : * \)

4: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{Dep} : * \)

5: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{Dep} : * \)

7: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{Dep} : * \)

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10: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{PEP} : * \)

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12: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{PEP} : * \)

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17: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{PEP} : * \)

18: \( \cgn2 \frac{6}{\prodata} \) \( \text{Pubpaa} \) \( \text{USOF} \) \( \text{PUBCOMB} \) \( \text{PEP} : * \)

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19: \( \cgn2 \frac{6}{\prodata} \) \( \text{PUBDaa} \) \( \text{PUBCOMB} \) \( \text{PEP} : * \)

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-184-634-477
US-10-123-155-81
US-10-146-731-81
US-10-146-731-81
US-10-140-472-81
US-10-141-761-81
US-10-141-761-81
US-10-141-885-81
US-10-141-885-81
US-10-138-790-81
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-10-140-923-81

US-10-141-756-81

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US-10-140-864-81

US-10-140-864-81

US-10-140-864-81

US-10-140-864-81

US-10-741-79-177

US-10-123-155-491

US-10-123-155-491

US-10-146-731-491

US-10-146-731-491

US-10-146-731-491

US-10-146-731-491

US-10-146-865-491

US-10-140-865-491

US-10-140-865-491

US-10-140-864-491

US-10-142-464-585

US-10-142-464-585

US-10-144-759-233

US-10-144-751-233

US-10-146-731-233

US-10-146-731-233

US-10-142-863-233

US-10-142-863-233

US-10-142-863-233

US-10-142-863-233

US-10-142-885-233

US-10-142-885-233

US-10-142-885-233

US-10-142-885-233

US-10-153-153-233
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#### ALIGNMENTS

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Sequence 125. Application US/10363204
Sublication No. US20040170955A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TILE REFERENCE: 005774. P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
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LOCATION: (1)..(31);
CTHER INFORMATION: synthetic construct
US-10-363-204-125
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ORGANISM: Artificial Sequence
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US-10-363-204-125
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US-10-307-817-562
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Matches 31
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LENGTH: 3288
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APPLICANT: Analy, Zemin
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT PILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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    TITLE OF INVENTION: WOULD PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
LENGTH: 3147
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Publication No. US20040058338A1
GENERAL INFORMATION:
APPLICANT: Age et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307, 817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSequist version 0.1
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Pred. No. 36;
2; Mismatches
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Publication No. US20030044930A1
GENERAL INFORMATION:
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Best Local Similarity 41.9%;
Matches 13; Conservative
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 41.99
Matches 13; Conservative
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                                                                                                                                                                         TYPE: PRT

ORGANISM: Homo sapiens

US-10-307-817-562
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APPLICANT: Agee et al
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US-10-184-644-477
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LENGTH: 3147
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/184,634
CURRENT APPLICANTION NUMBER: US/10/184,634
CURRENT PILING DATE: 2002-06-28
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Publication No. US20030195156A1
GENERAL INFORMATION:
APPLICANT: MIN, HOSUNG
APPLICANT: ATTLE OF INVENTION:
TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
FILE REPRENCE: A-743
CURRENT APPLICATION NUMBER: US/10/145,206
CURRENT APPLICATION NUMBER: US 60/290,196
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
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                                                                                    Score 71; DB 14; Length 3288; Pred. No. 37; 2; Mismatches 6; Indels
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SEQ ID NO 477
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SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 7285
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ORGANISM: Artificial Sequence
                                                                                         ich 35.9%;
il Similarity 57.9%;
11; Conservative
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ORGANISM: Homo Sapien
TYPE: DNA
ORGANISM: Homo Sapien
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Matches 11; Conserv
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                                          US-10-184-644-477
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERRINGE: 9330R1C323
CURRENT APPLICATION NUMBER 2002-05-15
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
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Pred. No. 47;
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NUMBER OF SEQ ID NOS: 550
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44.4%; Pred. No. 47;
tive 1; Mismatches
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1; Mismatches
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Publication No. US20030138888A1
GENERAL INFORMATION:
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Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                   Stewart, Timothy A.
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Smith, Victoria
Stewart, Timothy A.
                                                                                                                    Tumas, Daniel
Watanabe, Colin K
Wood, William
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
                                         Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 44.4'
Matches 12; Conservative
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Filvaroff, Ellen
                                                                              Smith, Victoria
Goddard, Audrey
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ORGANISM: Homo Sapien
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CORGANISM: Homo Sapien
US-10-140-472-81
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APPLICANT:
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                                     NAME/KEY: misc_feature
OTHER INFORMATION: Xaa (Pos1,2,3,15,16,17) are each independently absent or amino oTHER INFORMATION: id residues;
OTHER INFORMATION: Xaa (Pos5,6,7,9,13) are each independently amino acid residues.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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                                                                                                                                                             DB 14;
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Best Local Similarity 40.0%; Pred. No. 78;
Matches 14; Conservative 1; Mismatches
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OTHER INFORMATION: pAMG21-RANK-Fc vector
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Godowski, Paul J.
Gurney, Austin L.
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DeForge, Laura
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Gerritsen, Mary E
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Filvaroff, Ellen
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APPLICANT: Beredini, Mauree
APPLICANT: Deforge, Laura
APPLICANT: Pilvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Mei-Qiang
APPLICANT: Gerifeen, Mary
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; ORGANISM: Homo Sapien
US-10-123-155-81
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 3233
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CURRENT FILING DATE: 2002-05-10
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LENGTH: 3233
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C248
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333041198
CURRENT APPLICATION NUMBER: 105/10/141,761
CURRENT PILING DATE: 2002-05-08
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744 CCTACCTTCCAGGACCTCCTGGCCTGC 770
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                                                                                       Sequence 81, Application US/10141761 Publication No. US20030148432A1 GENERAL INFORMATION:
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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US-10-141-761-81
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LENGTH: 3233
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R10448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
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Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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Pred. No. 47;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             US-10-158-790-81
; Sequence 81, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao, Weil-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarceff, Ellen
APPLICANT: Gao, Wei-Qiang
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
                                                                                           TYPE: DNA
ORGANISM: Homo Sapien
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US-10-141-756-81
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                                                                                                   ALFLICANT: Zhang, Zemin

TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT APPLICATION NUMBER: US/01/137,871
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTHE
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
LENGTH: 3233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      744 CCTACCTTCCAGGACCTCCTGGCCTGC 770
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Publication No. US20030207355A1
GENERAL INFORMATION:
                                                          Smith, Victoria
Stewart, Timothy A.
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Gerritsen, Mary E.
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-137-871-81
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CORGANISM: Homo Sapien
US-10-140-923-81
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C200
CURRENY APPLICATION NUMBER: US/10/141,756
CURRENY TILING DATE: 2000-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 81
LENGTH: 3233
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Sequence 81, Application US/10141756
Publication No. US20030207359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                      Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Desnoyers, Luc
Filvaroff, Ellen
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Gerritsen, Mary E.
                                                                                                          Beresini, Maureen
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Gurney, Austin L.
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; ORGANISM: Homo Sapien
US-10-141-756-81
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Query
Result
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5: (cgm2 6/ptodata/1/paa/USO8 COMB.pep:*
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                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CYNLCIRECESICGADGACWTWCADGCSRSC 31
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
Sequence:
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Maximum DB &
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Searched:

Run on:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ΩI	Description
			į		TOTAL MODEL TO THE PARTY OF THE	
- 7	198	100.0			PCT-US01-2/832A-123	equence
М	198	100.0			US-10-363-204-125	Sequence 125, App
47 L	198	100.0		33	US-10-784-537-1	Sequence 1, Appli
n va	130	3.6			DCT-11503-26780-3256	Segmence 37, Appril
	5.5	36.9			PCT-US03-26780-3258	Sequence 3258, Ap
œ	73	36.9			PCT-US03-26780-3257	Seguence 3257, Ap
σ,	71.5	36.1			PCT-US03-26780-3056	Sequence 3056, Ap
10	71	35.9			PCT-US03-26780-2634	Sequence 2634, Ap
11	7 5	25.0			PCT-USU3-26/80-2636	Sequence 2637, Ap
13	7.7	35.9			PCT-USO3-26780-2637	Sequence 2690, Ap
14	71	35.9			PCT-US03-26780-2697	Sequence 2697, Ap
15	71	35.9			PCT-US03-26780-2699	Sequence 2699, Ap
16	71	35.9			PCT-US03-26780-2710	Sequence 2710, Ap
17	Ε.	35.9			PCT-US03-26780-2718	Sequence 2718, Ap
0 6	7.7	35.9			PCT-11S03-26780-2763	Sequence 2563. Ap
50 7	71	35.9			PCT-US03-26780-2747	Sequence 2747, Ap
21	71	35.9			US-10-307-817-562	Sequence 562, App
22	71	35.9		29	US-10-307-817-563	Sequence 563, App
23	71	35.9		36	US-60-592-191-182	Sequence 182, App
24	71	35.9		27	US-10-176-912-477	Sequence 477, App
225	7.7			7 6	US-IO-I/9-524-4//	Sequence 4//, App
9 70	7 5	20.0		7 2	US-10-164-654-4// IIS-10-184-644-477	Sequence 477, App
28.	7.17	35.9		36	US-60-592-191-185	Sequence 185, App
29	71	35.9		36	US-60-592-191-190	Sequence 190, App
30	71	35.9		36	US-60-592-191-189	Sequence 189, App
31	70.5	35.6		н :	PCT-US02-15273-28	Sequence 28, Appl
32	70.5	35.6		27	US-10-145-206-28	Sequence 28, Appl
333	2.07	35.6		7 -	US-10-145-206A-28 pcr-ms03-26780-2628	Sequence 28, Appl
	200	3.0		٠.	PCT-US03-26780-2628	Sequence 2631. Ap
36	2 2	35.4			PCT-US03-26780-2604	Sequence 2604, Ap
37	70	35.4		27	US-10-137-871-81	Sequence 81, Appl
38	70	35.4		27	US-10-158-790-81	Seguenc
39	0, 10	35.4		<b>,</b> ,	PCT-US04-07434-47	ednence
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4.2	69.5	35.1		3 6	US-10-741-790-177	Sequence 177, App
43	69.5	35.1			σ	Sequence 2908, Ap
4. 4 4. 1	69.5	35.1	2700	1 26	PCT-US03-26780-2909 US-10-063-545-79	Sequence 2909, Ap Sequence 79, Appl
2	5				100000	- Add - Company
					ALIGNMENTS	
RESULT 1						
PCT-US01	1-27692A	-125	•	į		
; Sequer	ice 125,	Applic	cation P	Č/	US0127692A	
, GENERA	CANT B	MATION:	Regent	ď	v of Texas	stem
TITLE	OF INVI	ENTION	Human	and	ing Peptide	s Identified by Phage Display
FILE	REFEREN	CB: 005	5774.P00	3 P.C.1	,	
, CURRE	INT APPL.	ICATION	N NUMBER	٠. ۳	; CURRENT APPLICATION NUMBER: PCT/US01/27692A	
, CURRE	SNT FILLI	אק הדיר	2001	-0.5	-0.7	
SOFTW	TARE: Pat	tentin	version	3.1		
; SEQ IL	NO 125					
, LENG	3TH: 31					
TYPE	TYPE: PRT OPCANIEM: Artificial	4 4 4 4 5 5 5	1000	200	á	
: FEATURE	URE:		iai sequence	2	n	
NAME	3/KEY: Pe	eptide				
LOCA	LOCATION: (1)(31)	1) (3]	[ ) 0.mtbo		1	
CT-US01	; OTHER INFORMATI PCT-US01-27692A-125	MATION: -125	: Вулспе	C1C	synthetic construct	

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APPLICANT: ARAP, WADIH
APPLICANT: PASQUALINI
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TITLE OF INVENTION: AMINOPEPTIDASE A (APA) TARGETING PEPTIDES
TITLE OF INVENTION: POR THE TREATMENT OF CANCER
FILE REPERENCE: UTSC: 912US
CURRENT PILING DATE: 2004-02-23
PRIOR PILING DATE: 2002-08-30
PRIOR PELING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PELING DATE: 2001-09-07
PRIOR PELING DATE: 2001-09-07
PRIOR PELING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-784-537-9
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US-10-363-204-125

Sequence 125. Application US/10363204

GENERAL INFORMATION:

APPLICANT: Board of Regents, The University of Texas System

TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display

TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display

TITLE OF INVENTION NUMBER: US/10/363,204

CURRENT APPLICATION NUMBER: US/10/363,204

CURRENT FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 251

SOFTWARE: PatentIn version 3.1
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                                 100.0%; Score 198; DB 1; Length 31; 100.0%; Pred. No. 4.3e-14; tive 0; Mismatches 0; Indels
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I.OCATION: (1)..(31);
OTHER INFORMATION: synthetic construct
US-10-363-204-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Peptide PCT-US02-27836-58
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                             Query Match
Best Local Similarity 100.
Matches 31, Conservative
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Gaps
Sequence 1, Application US/10784537

Sequence 1, Application US/10784537

Sequence 1, Application

APPLICANT: ARAP, WADIH

APPLICANT: ARAP, WADIH

APPLICANT: ALAUDENRANTA, JOHANNA

TITLE OF INVENTION: POR THE TREATMENT OF CANCER

TITLE OF INVENTION: POR THE TREATMENT OF CANCER

FILE REFERENCE: UTSC:8720S

CURRENT APPLICATION NUMBER: DCT/US02/27836

PRIOR FILING DATE: 2002-08-30

PRIOR FILING DATE: 2002-09-07

PRIOR FILING DATE: 2002-09-07

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-01-17

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-01-17

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Matches 31; Conservative 0; Mismatches
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TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF
TITLE OF INVENTION: THEIR USE
FILE REPERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
CURRENT FILING DATE: 2003-08-28
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GENERAL INFORMATION:
APPLICANT: FIVERENE THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE
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FRIOR PAPLICATION NUMBER: 60/406,655
FRIOR APPLICATION NUMBER: 60/406,642
FRIOR APPLICATION NUMBER: 60/406,640
FRIOR FILING DATE: 2002-08-29
FRIOR APPLICATION NUMBER: 60/406,588
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FRIOR APPLICATION NUMBER: 60/406,588
FRIOR APPLICATION NUMBER: 60/406,588
FRIOR APPLICATION NUMBER: 60/406,566
FRIOR FILING DATE: 2002-08-29
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FRIOR PLILING DATE: 2002-08-29
FRIOR PILING DATE: 2002-08-29
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FRIOR APPLICATION NUMBER: 60/406,656
FRIOR FILING DATE: 2002-08-29
FRIOR APPLICATION NUMBER: 60/406,653
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                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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45.2%; Pred. No. 67;
tive 1; Mismatches
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SEQ ID NO 9
LENGTH: 31
TYBE: PR
ORGANISM: Artificial Sequence
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Best Local Similarity 45.24
Matches 14; Conservative
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ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2003-08-8

PRIOR APPLICATION NUMBER: 60/406,616

PRIOR FILING DATE: 2002-08-29

PRIOR PILING DATE: 2002-08-29

PRIOR PLING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,666

PRIOR PRIOR APPLICATION NUMBER: 60/406,653

PRIOR PLING DATE: 2002-08-29

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NUMBER OF SEQ ID NOS: 3700
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Best Local Similarity 45.2%
These 14; Conservative
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TYPE: PRT
ORGANISM: Homo
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          CURRENT
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Matches
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APPLICANT: FIVERENEUE THERAPEUTICS, INC.

TITLE OF INVENTION: HUMAN POLYBEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF

TITLE OF INVENTION: THEIR USB

FILE REPERENCE: 08940. 0014-00304

CURRENT PILING DATE: 2003-08-28

FRIOR PELICATION NUMBER: 60/406,616

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 2002-08-29

PRIOR PELICATION NUMBER: 60/406,655

PRIOR PELICATION NUMBER: 60/406,642

PRIOR PELICATION NUMBER: 60/406,642

PRIOR PELICATION NUMBER: 60/406,640

PRIOR PELICATION NUMBER: 60/406,646

PRIOR PELICATION NUMBER: 60/406,666

PRIOR PELICATION NUMBER: 60/406,663

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GENERAL INFORMATION:
APPLICANT: FIVEPRIME THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYREPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE
PILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PCT/US03/26780
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                                                                                                                                                                                                                                36.9%; Score 73; DB 1; Length 4848; ilarity 45.2%; Pred. No. 1e+02; Conservative 1; Mismatches 14; Indels
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36.1%; Score 71.5; Di
Best Local Similarity 45.2%; Pred. No. 76;
Matches 14; Conservative 1; Mismatches
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3257
LENGTH: 4848
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PCT-US03-26780-3056
                                                                                                                             ORGANISM: Homo sapiens
PCT-US03-26780-3257
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Best Local Similarity
Matches 14; Conserv
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SOFTWARE: Pater
SEQ ID NO 3056
LENGTH: 2027
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF

TITLE OF INVENTION: HTHEIR USB

FILE REFERENCE: 08940.0014-00304

CURRENT APPLICATION NUMBER: PCT/US03/26780

CURRENT FILING DATE: 2003-08-28

PRIOR FILING DATE: 2002-08-29

PRIOR PELING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,555

PRIOR APPLICATION NUMBER: 60/406,640

PRIOR PILING DATE: 2002-08-29

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PRIOR APPLICATION NUMBER: 60/406, 616
PRIOR PLILNG DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PLILNG DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406, 559
PRIOR APPLICATION NUMBER: 60/406, 642
PRIOR PILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
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SEQ ID NO 2636
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PCT-US03-26780-2690
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APPLICANT: FYTERIME THERAPEUTICS, INC.

1TITLE OF INVENTION: HUMAN POLYEPPIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYEPPIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: HUMBER: PCT/US03/26780 CURRENT FILID MADER: 2003-08-28 PRIOR PELICATION NUMBER: PCT/US03/26780 CURRENT APPLICATION NUMBER: 60/406, 516 PRIOR PILING DATE: 2003-08-29 PRIOR PILING DATE: 2003-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR APPLICATION NUMBER: 60/406, 655 PRIOR APPLICATION NUMBER: 60/406, 640 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING DATE: 2002-08-29 PRIOR PILING PAPELICATION NUMBER: 60/406, 666 PRIOR APPLICATION PAPELICATION DATE: 2002-08-29 PRIOR PILING PAPELICATION PAPELICATION DATE: 2002-08-29 PRIOR PAPELICATION PAPELICATION DATE: 2002-08-29 PRIOR PAPELICATION PAPELICATION DATE: 2002-08-29 PRIOR PAPELICATION PAPELICATION DATE: 2002-08-29 PRIOR PAPELICATION PAPELICATION PAPELICATION DATE
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APPLICANT: FIVERENT HETAPEUTICS, INC.
TITLE OF INVENTION: THER USE
FILE REFERENCE: 08940.0014-00304
CURRENT FILENCE OF INVENTION WHERE: PARTHODS OF TITLE OF INVENTION WHERE PARTHONS OF TITLE OF INVENTION WHERE PARTHONS OF TITLE OF INVENTION WHERE PARTHONS OF CURRENT APPLICATION NUMBER: PARTHONS OF CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: 60/406,616
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                                                                                                                                                                                                          35.9%; Score 71; DB 1; Length 291; 57.9%; Pred. No. 19;
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                                                                                                                                                                                                                                                                                      2; Mismatches
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Best Local Similarity 57.99
Matches 11; Conservative
                                                TYPE: PRT; ORGANISM: Homo sapiens
PCT-US03-26780-2636
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LENGTH: 291
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PGT-1630-126780-12697, Application PC/TU80326780
GENERAL INFORMATION:
APPLICAMT: FIVEPRINE THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TITLE OF INVENTION: HTER USE
FILE U
FRIOR APPLICATION NUMBER: 60/406,655
PRIOR PILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR PLING DATE: 2002-08-29
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ORGANISM: Homo sapiens
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GENERAL INVORMATION:

APPLICANT: FIVERRIME THERAPEUTICS, INC.

TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE

FILE REPERENCE: 08940.0014-00304

CURRENT APPLICATION NUMBER: PCT/US03/26780

CURRENT PILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,616

PRIOR PILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR PLING DATE: 2002-08-29

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                                                                                                               Query Match 35.9%; Score 71; DB 1; Length 659; Best Local Similarity 57.9%; Pred. No. 36; Matches 11; Conservative 2; Mismatches 6; Indels
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SEQ ID NO 2699
LENGTH: 659
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PCT-US03-26780-2699
; ORGANISM: Homo sapiens
PCT-US03-26780-2697
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PCT-US03-26780-2699
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Search completed: November 16, 2004, 14:46:42 Job time : 506.943 secs

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Sequence 48, Application US/10411910B
Sequence 48, Application US/10411910B
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
TITLE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910B
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 363
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
ILENGTH: 844
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US-10-411-910B-48
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US-10-489-071-60
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Sequence 56, Appl
Sequence 56, Appl
Sequence 105, Appl
Sequence 27, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 13625, A
Sequence 13625, A
Sequence 104, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 20, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 2751, Appl
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Sequence 14189, A
Sequence 14197, A
Sequence 14188, A
Sequence 14210, A
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                                                                                           November 16, 2004, 14:24:42; Search time 5.88679 Seconds (without alignments) 40.083 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-411-910B-48

US-10-489-071-56

US-10-489-071-56

US-10-983-693B-105

US-10-976-102-52

US-10-846-989-57

US-10-846-989-57

US-10-846-989-57

US-10-976-102-89

US-10-976-102-89

US-10-976-102-89

US-10-976-102-89

US-10-973-923-1365

US-10-10-101-72

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US-10-10-101-101-73

US-10-10-101-73

US-10-732-923-9253

US-10-732-923-14189

US-10-732-923-14189

US-10-732-923-14189

US-10-732-923-14189
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                                                                                                                                                                                                                                                                             80665 seqs, 18150633 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                            1 CPKVCPRECESNC 13
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Maximum DB seq length: 200000000
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84
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Match Length
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Sequence 60, Application US/10489071
GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OP USE OF TARGETING PEPTIDES AGAINST:
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 13
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                                                                                                Sequence 1204, Ap
Sequence 1, Appli
Sequence 14190, A
Sequence 14191, A
                     14218, A
65, Appl
14308, A
5576, Ap
5350, Ap
                                                                                                                                                                           833, App
2, Appli
97, Appl
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5731, Ap
                                                                                       842, App
                                                                                                                                         Sequence 78, Appl
Sequence 79, Appl
Sequence 96, Appl
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US-09-978-191B-363
US-10-799-829B-363
US-10-792-923-14218
US-10-276-102-65
US-10-220-366A-14308
US-10-732-923-5576
US-10-732-923-5576
US-10-732-923-5545
US-10-732-923-15545
US-10-732-923-1204
US-10-732-923-14190
US-10-732-923-14191
US-10-776-102-79
US-10-976-102-79
US-10-976-102-79
US-10-976-102-79
US-10-976-102-79
US-10-976-102-79
US-10-976-102-98
US-10-976-103-93
US-10-976-103-93
US-10-988-97
US-10-988-97
                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Peptide US-10-489-071-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CPKVCPRECESNC 13
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                                                                         ##PEPLICANT: COGAL.
##PEPLICANT: COGAL.
### APPLICANT: COGAL.
### TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
### TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
### FILE REFERENCE: 00786/351004
### CURRENT APPLICATION NUMBER: US/09/205,658
### CURRENT FILING DATE: 2001-09-25
### PRIOR PEPLICATION NUMBER: US/09/205,658
### PRIOR PELLING DATE: 1998-12-03
### PRIOR APPLICATION NUMBER: 08/885,7076
### PRIOR APPLICATION NUMBER: 08/889,534
### PRIOR APPLICATION NUMBER: US98/10080
### PRIOR PELLING DATE: 1999-05-15
### PRIOR PELLING DATE: 1999-05-15
### NUMBER OF SEQ ID NOS: 331
### SOFTWARE: PASESEQ for Windows Version 4.0
### ILENGTH: 383
### ILENGTH: 383
### ILENGTH: 383
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Sequence 52, Application US/10976102

GENERAL INFORMATION:
APPLICANT: Slamons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT FILING DATE: 2004-10-27
PRIOR PPLICATION NUMBER: 09/950,933
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-13
NUMBER: OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 383;
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7.4;
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Pred. No. 7.4;
2; Mismatches
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GENERAL INFORMATION:
APPLICANT: BDDMEN, MARK WILLIAM
APPLICANT: BRIEND, EWARNUEL CYRILLE PASCAL,
APPLICANT: CHAMPION, BRIAN ROBERT
                     Sequence 105, Application US/09963693B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Drosophila melanogaster
US-09-963-693B-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.0%;
Best Local Similarity 46.2%;
Matches 6; Conservative 2
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; ORGANISM: Triticum aestivum
US-10-976-102-52
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Matches 7; Conservative
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                                             GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
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US-10-765-727-23
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SEQUENCE 56, Application US/10489071

GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
FILLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
CURRENT APPLICATION NUMBER: US/10/489,071

CURRENT APPLICATION NUMBER: PCT/US02/27836
PRIOR PILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144

SEQ ID NOS: 144

SEQ ID NO 56
LENGTH: 9
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Sequence 58, Application US/10489071

Sequence 58, Application US/10489071

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES

CURRENT APPLICATION NUMBER: US/10/489,071

CURRENT FILING DATE: 2004-03-08

PRIOR FILING DATE: 2004-03-08

NUMBER OF SEQ ID NOS: 144

SEQ ID NO 582 ID NOS: 131

LENGTH: 31
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                  Score 53; DB 6; Length 844;
Pred. No. 2.4;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 6; Length 9; Pred. No. 7.4e+04; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Peptide US-10-489-071-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Peptide US-10-489-071-58
                     63.1%;
53.8%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                            177 CGRVCPHSCEAQC 189
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                                                                                                               1 CPKVCPRECESNC 13
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Matches 8; Conservative
                                                                  Conservative
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Query Match
Best Local Similarity
7; Conserve
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RESULT 5 US-09-963-693B-105

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Sequence 3, Application:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: LAL, Preet.
APPLICANT: CORLEY, Neil C.
             Application US/10883805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 CPPKCPPQCPAPC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPKVCPREC 9
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Matches
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HILE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
FILE REPERENCE: 674525-2010
CURRENT APPLICATION NUMBER: US/10/765,727
CURRENT PILING DATE: 2004-01-23
FRIOR PILING DATE: 2002-07-25
FRIOR APPLICATION NUMBER: PCT/GB02/03426
FRIOR APPLICATION NUMBER: GB 0118153.6
FRIOR PILING DATE: 2002-07-25
FRIOR PILING DATE: 2002-04-05
FRIOR PILING DATE: 2002-04-05
FRIOR PILING DATE: 2002-04-05
FRIOR FILING DATE: 2002-04-05
FRIOR FILING DATE: 2002-05-28
FRIOR FILING DATE: 2002-05-28
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Pred. No. 58;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TUGAL, TAMARA
APPLICANT: TUGAL, TAMARA
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MEDICAL TREATMENT
FILE REPERENCE: 654525-2012
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PT/GB02/05133
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2001-11-14
PRIOR PLILNG DATE: 2001-11-14
PRIOR PLILNG DATE: 2001-11-14
PRIOR PLILNG DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: RACKNZIE, GRAHAME JAMES
APPLICANT: RAGNO, SILVIA
APPLICANT: TUGAL, TAMARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-846-989-57; Sequence 57, Application US/10846989; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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SOFTWARE: PatentIn Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPKVCPRECESNC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-846-989-57
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LENGTH: 2471
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LENGTH: 2471
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GENERAL INFORMATION:
APPLICATION:
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Pred. No. 4.3;
2; Mismatches
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Pred. No. 46;
0; Mismatches
APPLICANT: CUCLER, WAIT U.
APPLICANT: GUEGLER, WAIT U.
APPLICANT: BAUGHN, MAXIAH R.
APPLICANT: BAUGHN, MAXIAH R.
APPLICANT: TUE, Henry
TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
TITLE OF INVENTION: HUMAN EPIDERMAL PROTEINS
TILLE REPERENCE: PF-0567 PCT
CURRENT APPLICATION NUMBER: 09/123,531
PRIOR APPLICATION NUMBER: 09/123,531
PRIOR APPLICATION NUMBER: 09/206,817
PRIOR APPLICATION NUMBER: 09/206,817
PRIOR FILING DATE: 1998-12-07
PRIOR FILING DATE: 1998-12-07
PRIOR FILING DATE: 1998-12-07
PRIOR FILING DATE: 1998-12-07
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: PERL PROGRAM
TENCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc feature
; OTHER INFORMATĪON: Incyte Clone No: 1798487
US-10-883-805-3
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US-10-732-923-13625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 1370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn version 3.2
                                                                                                                                                               Query Match 52.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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215 CQKVCPTICKSH 226
                                                                                                                                                                                                                                                                                       215 COKVCPTICKSH 226
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                               1 CPKVCPRECESN 12
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 2768
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TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/963,693B
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/26,658
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 08/888,534
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-15
                       APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 1278D
CURRENT APPLICATION NUMBER: US/10/976,102
CURRENT FILING DATE: 2004-10-27
PRIOR RAPLICATION NUMBER: 09/950,933
PRIOR RILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.4%; Score 44; DB 5; Length 370; 58.3%; Pred. No. 18; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 6; Length 80;
Pred. No. 4.4;
2; Mismatches 4; Indels
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TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00
CURRENT PEPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 331
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Application US/09963693B
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 229, Application US/10482029; GENERAL INFORMATION:
        APPLICANT: Navarro Acevedo, Pedro A.
                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-976-102-89
                                                                                                                                                                                                                                                                                                                                                                                            52.4%;
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Best Local Similarity 58.3.
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Best Local Similarity 50.0
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-963-693B-104
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US-09-963-693B-104
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US-10-482-029-229
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LENGTH: 370
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APPLICANT: Clinton, Gail
APPLICANT: Roberts, Charles T
TITLE OF INVENTIONS: COMPOSITIONS AND METHODS FOR TREATING DISEASE
FILE REFERENCE: 49321-125
CURRENT PELLING NUMBER: US/60/616,596
CURRENT FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 1382
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LOCATION: (734)...(734)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; Sequence 72, Application US/10510101
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John
; APPLICANT: Fikes, John
; APPLICANT: Fikes, John
; APPLICANT: Gette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT PILING DATE: 2004-10-05
; PRIOR PILING DATE: 2002-09-26
; PRIOR PILING DATE: 2002-09-26
; PRIOR PILING DATE: 2002-09-05
; RIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOPPLWANDE: DATE: 2002-04-05
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Score 44; DB 6; Length 1370;
Pred. No. 63;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                        US-60-616-596-20; Sequence 20, Application US/60616596; GENERAL INFORMATION:
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COTHEN INFORMATION: Xaa can be any naturally occurring amino acid prints INFORMATION: Xaa can be any naturally occurring amino acid name/KEX: misc feature correctly conservation: (2501). (2501) OCHER INFORMATION: Xaa can be any naturally occurring amino acid us-10-510-101-72 Correctly Match 52.4%; Score 44; DB 6; Length 2768; Best Local Similarity 77.8%; Pred. No. 1.20+02; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Search completed: November 16, 2004, 14:47:13 Job time : 6.88679 secs

2 PKVCPRECE 10 || || || || 157 PKRCPRSCE 165

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 16, 2004, 14:15:03 ; Search time 14.717 Seconds (without alignments) 84.991 Million cell updates/sec Run on:

US-10-784-537-3 84

1 CPKVCPRECESNC 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRAMADIES

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	ВВ	ID	Description
	54	64.3	1363	7	T43220	insulin-like growt
7	53	63.1	425	~	AE2094	hypothetical prote
m	52	61.9	413	~	JE0142	8
4	51	60.7	468	~	H72230	glutamate synthase
2	20	59.5	51	Н	XKPOT	proteinase inhibit
9	20	59.5	105	~	G95318	FdxB ferredoxin II
7	20	59.5		N	JE0352	mucin MUCSB, trach
80	20	59.5		N	T23681	hypothetical prote
σ,	49	58.3		~	A70477	8
10	49	58.3		~	A46602	glutamate synthase
11	49	58.3		N	D87696	glutamate synthase
12	48	57.1		~	B41132	collagen-related p
13	47	56.0		Н	FERF3C	ferredoxin 2[4Fe-4
14	47	26.0		~	H85852	probable oxidoredu
15	47	56.0		~	A64983	hypothetical prote
16	47	56.0		N	F91008	probable oxidoredu
17	47	56.0		0	S57245	insulin receptor (
18	47	56.0	7	Н	A56081	insulin receptor -
19	46	54.8	204	~	T08072	proteinase inhibit
20	46	54.8		~	T09288	late embryonic abu
21	46	54.8		~	T31887	hypothetical prote
22	46		388	N	T31888	
23	46	54.8	395	N	S75952	
24	46	•	438	~	T31889	
25	46	₹.	445	~	T31898	
56	46	4	573	~	JC4335	ಹ
27	45	۳.	342	N	T16735	hypothetical prote
28	45	٠	471	N	$\sim$	
59	45	53.6	472	7	G85985	glutamate synthase

glutamate synthase	glutamate synthase	glutamate synthase	glutamate synthase	NADH-glutamate syn	glutamate synthase	probable oxidoredu	hypothetical prote	proteinase inhibit	proteinase inhibit	trypsin inhibitor-	probable gibberell	proteinase inhibit	proteinase inhibit	proteinase inhibit	glutamate synthase
AB0907	D91140	G65112	AG0432	B89813	H82523	AF0042	T20561	T07597	TIEO1	JQ2269	A84713	S24973	S43105	JQ2153	E86785
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		~	~	_											
472	472	47	47	48	494	671	728	158	52	53	103	147	154	397	479
	53.6 472									52.4 53					

## ALIGNMENTS

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insulin-like growth factor-1 receptor - common lancelet
NiAlternate names: insulin-like peptide receptor
CiSpecies: Branchiostoma lanceolatum (common lancelet)
CiSpecies: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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Claces in 19320 Regimes—revision in control of a control

Gaps ö Length 1363; 5; Indels Score 54; DB 2; Pred. No. 8.6; 0; Mismatches Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative (

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hypothetical protein alr2308 (imported) - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004
C;Aacession: AE2094
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2094
A;Accession: AE2094
A;Accession: AE2094
A;Accession: AE2084
A;Accession: AE2085
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A;Accession: A

A;Cross-references: UNIPROT:QBYUN1; GB:BA000019; PIDN:BAB74007.1; PID:gl7131400; GSPDB:Gl A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr2308

Gaps ö Query Match 63.1%; Score 53; DB 2; Length 425; Best Local Similarity 61.5%; Pred. No. 5.1; Matches 8; Conservative 0; Mismatches 5; Indels

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Biochemistry 21, 752-756, 1982
A;Title: Primary structures of two low molecular weight proteinase inhibitors from potatc
A;Reference number: A90465; WUID:82182863; PMID:7074039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: G95318
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowst, Kalbarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Froc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot: A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: 0922X89; GB: AB: D006469; PIDN: AAK65113.1; PID: g14523551; GSPDB: GB; Experimental source: strain 1021, megaplasmid pSymA sigaliber. P: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A; Reference number: As6039; MUID: 21368234; PMID: 11474104
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Biochem. Biophys. Res. Commun. 251, 350-355, 1998
A;Title: The amino-terminal sequence of MUCSB contains conserved multifunctional D domain A;Reference number: JE0352; MUID:99009274; PMID:9790959
A;Accession: JE0352
A;Molecule type: mRNA
A;Residues: 1-1321 <OFF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
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C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                              A,Accession: A01318
A,Molecule type: protein
A,Rolidues: 1-51 (4MAs)
A,Cross-references: UNIPROT:P01079
A,Note: Arg-38 is probably the site of interaction with trypsin C,Superfamily: potero proteinase inhibitor PTI
C,Keywords: serine proteinase inhibitor
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Pred. No.
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                                                                                                                                                                                                                                                                                                     59.5%;
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C;Species: Sinorhizobium meliloti
                                                                                                                                                                                                                                                                                                  Query Match 59.5
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             2 PKVCPRECESN 12
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CARVCPRDCQTH
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A;Molecule type: DNA
A;Residues: 1-105 <KUR>
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C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H72230
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glutamate synthase (EC 1.4.1.-) small chain - Rhodobacter sphaeroides C; Species: Rhodobacter spaeroides C; Species: Rhodobacter spaeroides C; Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004 C; Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004 C; Accession: JE0142 B; Lu, T.; Wu, Y.Q.; Song, H.Y. Accession: JE0142 B; Lu, T.; Wu, Y.Q.; Song, H.Y. Accession: JE0142 A; Reference number: JE0142 A; Reference number: JE0142 A; Residues: 1-413 <-LUAA A; Residues: 1-413 <-LUAA A; Residues: 1-413 <-LUAA A; Residues: Ludaa A; Mote: the authors translated the codon CTG for residue 24 as Lys, CAC for residue 30 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72230
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C;Species: Solanum tuberosum (potato)
C;Daccies: Solanum tuberosum (potato)
C;Daccesion: A01118
R;Hass, G.M.; Hermodson, M.A.; Ryan, C.A.; Gentry, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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6.8;
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Pred. No. 10;
2; Mismatches
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Pred. No. 6.8;
3; Mismatches
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A;Gene: TM1640
C;Superfamily: glutamate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: gltD
C;Superfamily: glutamate synthase small chain
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 61.9%;
Similarity 53.3%;
8; Conservative
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                                                                                    108 CPSDCPRPCEKIC 120
                               CPKVCPRECESNC 13
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Best Local Similarity
Matches 9; Conserv
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Gaps

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Glutamate synthase (NADPH) (EC 1.4.1.13) beta chain [validated] - Azospirillum brasilens C; Species: Azospirillum brasilense C; Species: Azospirillum brasilense C; Species: Azospirillum brasilense C; Species: Azospirillum brasilense C; Species: Azospirillum brasilense 16-Aug-2004 (C; Azocssion: A46602; S10765; S51164 (R; Pelanda, R.; Vanoni, M.A.; Perego, M.; Piubelli, L.; Galizzi, A.; Curti, B.; Zanetti, A; Elo. Chem. 268, 3099-3106, 1993 (A; Piubelli, L.; Galizzi, A.; Curti, B.; Zanetti, A; Title: Glutamate synthase genes of the diazotroph Azospirillum brasilense. Cloning, se A; Reference number: A46602; MUID:93155143; PMID:8428988
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q05756; GB:L04300; NID:g289243; PIDN:AAA22178.1; PID:g304130 A;Experimental source: strain Sp7, strain ATCC 29145 and strain Sp6 A;Note: sequence extracted from NCBI backbone (NCBIN:124365, NCBIP:124371) R;Vanoni, M.A.; Negri, A.; Zanetti, G.; Ronchi, S.; Curti, B. Biochim. Biophys. Acta 1039, 374-377, 1990 A;Title: Structural studies on the subunits of glutamate synthase from Azospirillum bras A;Reference number: S10764; MUID:90335272; PMID:2198943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: protein
A, Residues: 2-19, X, 21-24;328-332, A, 334-336, X, 338, X, 340, X, 342, X, <VANI>
A; Residues: 2-19, X, 21-24;328-332, A, 334-336, X, 338, X, 340, X, 342, X, <VANI>
By, Vanoni, M.A.; Mazzoni, A.; Funagalli, P.; Negri, A.; Zanetti, G.; Curti, B.
Eur. J. Blochem. 226, 505-515, 1994
A, Title: Interdomain loops and conformational changes of glutamate synthase as detected A, Reference number: S51033; MUID:95094808; PMID:8001567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gluciante synthase, small subunit [imported] - Caulobacter crescentus
Gluciae: Caulobacter crescentus
Gluciae: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
Gluciae: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
Gluciae: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
Gluciae: Allorent W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Recession: D97696
A;Scatus: prellminary
A;Molecule type: DNA
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Description: catalyzes the NAD(P)H-dependent reductive transfer of L-glutamine amide c
C,Superfamily: Glutamate synthase, small subunit
C,Keywords: 3Fe-4S; iron-sulfur protein; metalloprotein; NADP; oxidoreductase
F;48,51,56,60,95,99,105,109/Binding site: iron-sulfur clusters (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.3%; Score 49; DB 2; 46.7%; Pred. No. 19; ative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CC3606
C,Superfamily: Glutamate synthase, small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::||:: || || CGRICPQDRLCEGNC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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Best Local Similarity 46.72
February 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 2-8;475-481 <VAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA; protein A; Residues: 1-481 <PEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPKVCPRB--CESNC
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Best Local Similarity
7, Conserve
                                                                                                                                                                                                                                                                                                                                        A; Accession: A46602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S10765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S51164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
A;Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927
C;Comment: This protein is large multimeric glycoproteins which is secreted by epithelia
C;Genetics:
A;Gene: MUC5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamate synthase small subunit gltD - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Aug-2004
C;Accession: A70477
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:067845; GB:AE000770; NID:92984274; PIDN:AAC07800.1; PID:9298
A,Experimental source: strain VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: 281573; PIDN: CAB04625.1; GSPDB: GN00020; CESP: MQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Gene: CESP:M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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                                                                                                                                                                    59.5%; Score 50; DB 2; Length 1321; 47.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 2; Length 1513;
Pred. No. 31;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 476;
                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:017970; EMBL:Z81573; PI
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Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1996
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                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                    ||::||| | ||
321 CPELCPRTCTNMQHQNC 337
                                                                                                                                                                                                                                                                                                1 CPKVCPREC----ESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone M02G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 CGRVCPQERQCEGSC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 CPKACMPECSNOC 1029
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                                                                                                                                                                                                                                     Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                               Query Match
Best Local Similarity
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Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 CARVCPTEKLCOSGC 87
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-412 <STO>
                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NiAlternate names: dimeric ferredoxin
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 08-Dec-1999 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: B32308; A46701
R;Moreno-Vivian, C:; Hennecke, S:; Puehler, A.; Klipp, W.
J. Bacteriol. 171, 2591-2598, 1989
A;Title: Open reading frame 5 (ORF5), encoding a ferredoxinlike protein, and nifQ are contraction b32308; MuID:89213944; PMID:2708314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA

A; Mosterial type: DNA

A; Residues: 1-102 <MOR>

A; Residues: 1-102 <MOR>

A; Cross-references: UNIPROT: P20624; GB: M26323; NID: G341472; PIDN: AAA26146.1; PID: G516637

B; Jouanneau, Y.; Meyer, C.; Gaillard, J.; Forest, E.; Gagnon, J.

B; Biol. Chem. 268, 1063-10644, 1993

A; Title: Purification and characterization of a novel dimeric ferredoxin (FdIII) from Rh

A; Reference number: A46701; MUID: 93252956; PMID: 8387524
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                                                                                                          RESULT 12
B41132
collagen-related protein 2 - Hydra magnipapillata (fragment)
c)Species: Hydra magnipapillata
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 15-Sep-2003
C;Accession: B41132; S21991
R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.
J. Cell Biol. 115, 1159-1169, 1991
A;Title: Mini-collagens in hydra nematocytes.
A;Reference number: A41132; MUID:92064646; PMID:1955459
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 «KUR»
A;Cross-references: EMBL:X61046; NID:g9448; PIDN:CAA43380.1; PID:g9449
A;Note: submitted to the EMBL Data Library, July 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 2; Length 142
Pred. No. 11;
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A, Note: sequence extracted from NCBI backbone (NCBIP:131349)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 57.1%;
Similarity 46.2%;
6; Conservative ;
| ::||:: || ||
94 CGRICPQDRLCEGNC 108
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
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| :||| ||::: 87 CARVCPSECQTH 98

> RESULT 14 . H85852

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85852
C;Accession: H85852
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q8X645; GB:AE005174; NID:g12516463; PIDN:AAG57284.1; GSPDB:GR
A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A64983
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science, D.J.; Mat, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-412 <BLAPT
A;Cross-treferences: UNIPROT:P76440; GB:AE000303; GB:U00096; NID:g1788456; PIDN:AAC75207...
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: Glutamate synthase, small subunit
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 16-Aug-2004
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31;
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Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.0%; Score 47; DB Best Local Similarity 53.3%; Pred. No. 31; Matches 8; Conservative 2; Mismatches
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A,Gene: Z3401
C,Superfamily: glutamate synthase small chain
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D.J.;
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08yunl anabaena sp
08rc72 thermoanaer
08rbw5 thermoanaer
07mbg7 wollinella s
074fu5 geobacter s
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Q73kq0 treponema d
Aa812687 treponema
Q8G114 synchococc
Q7mtd4 porphyromon
Q9x1x5 thermotoga
Q82x6 bacteroides
Q78547 neurospora
P01079 solanum tub
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Q84156 solanum phu
Aas01731 solanum p
O17970 caenorhabdi
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azospirillu
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                                                                                    November 16, 2004, 14:14:16; Search time 77.5094 Seconds (without alignments) 96.503 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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QBRBW5
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1: uniprot_sprot:*
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Q9rn12 zymomonas m
Q9hau2 homo sapien
Q724f5 homo sapien
Q9h7g8 homo sapien
Q00485 hydra sp. m
Q9h2q4 homo sapien
Q7u4k2 synechococc
Q8tjj7 methanosarc
Q748e7 geobacter s
Aar36449 geobacter
G6h27 rhodopseudo
Cae26122 rhodopseu
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 caulobacter
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Nature 419:512-519(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 419:512-519/2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Q9a2f9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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Hypothetical protein.
SEQUENCE 1359 AA; 158879 WW; FDBEC1141CCD176A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                   ALIGNMENTS
09A2F9
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07Z4F5
09H7G8
09H7G8
09H2Q4
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07H4K2
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01-MAZ-2004 (TrEMBLrel. 26, Last anno
18-65 cluster containing protein
Name=hycB, OrderedLocusNames=Prol714;
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Best Local Similarity 61.3,,
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                            Dufference A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin B.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Regorin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;

T. Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.";

T. Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

R. Ball, AB01166, AA000758.1;

E. Proc. Natl. Acad. Sci. U.S.A. in noning; IEA.

GO; GO:0005506; F:iron ion binding; IEA.

GO; GO:000518; P:electron transporter activity; IEA.

R. GO; GO:000518; P:electron transport; IEA.

R. Pfam; PF000071; Fer4; 1.
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002466;
001-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 44, Last annotation update)
05-UTL-2004 (Rel. 44, Last annotation update)
Insulin-like peptide receptor precursor (EC 2.7.1.112) (ILP receptor).
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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MEDLINE=96408719; PubMed=8813726;
Pashmforoush M., Chan S.J., Steiner D.F.;
"Structure and expression of the insulin-like peptide receptor from
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                      Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.3%; Score 54; DB 2; Length 331; 66.7%; Pred. No. 4.2; 3; Indels ive 1; Mismatches 3; Indels
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STRAIN-SARG / CCMP 1375 / SS120;
MEDLINE-22810154; Pubmed=12917486;
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Matches 8; Conservative
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      Prochlorococcus marinus.
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Cytoplasmic (Potential).
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Fibronectin type-III 4.
Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
Proton acceptor (By similarity).
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Pred. No. 16;
0; Mismatches
                                                  InterPro; IPR008957; FW_III-like.
InterPro; IPR006211; Furin-like.
InterPro; IPR006211; Furin-repeat.
InterPro; IPR006203; Grow_fac_recept.
InterPro; IPR001009; Kinase like.
InterPro; IPR000119; Prot_Kinase.
InterPro; IPR002011; RecepttyrkinalI.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
Fam; PF00041; fin3; 3.
Ffam; PF00067; Furin-like; 1.
Ffam; PF00069; PKinase, 1.
Ffam; PF00109; PKinase, 1.
Fram; PF010109; TYRKINASE.
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FN III.
FN III-like.
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EMBL; S83394; AAB50848.1;
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InterPro, IPR003961;
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SEQUENCE FROM N.A.

C STRAIN=MB4;

WEDLINE=21992816; PubMed=11997336;

WEDLINE=21992816; PubMed=11997336;

WEDLINE=21992816; PubMed=11997336;

WEDLINE=21992816; PubMed=11997336;

WEDLINE=21992816; PubMed=11997336;

A Tan H., Chen K., Wang Y., Xu J., Yang H.;

A Tan H., Chen R., Wang J., Xu J., Yang H.;

R Chen R., Wang J., Xu J., Yang H.;

R Chen R., Wang J., Xu J., Yang H.;

R Chen R., Wang J., Xu J., Yang H.;

R Chen R., Wang J., Xu J., Yang H.;

R Chen R., Wang J., Xu J., Yang H.;

R Gologe State Res 1.2 f89-700(2002).

R MSSP; Q28943; IGTE.

OR GO. GO:0015303; Polatifide oxidoreductase activity; IEA.

GO, GO:0015303; Pidita exidorase.

DR InterPro; IPR001327; FAD pyr redox.

DR InterPro; IPR001327; FAD pyr redox.

DR InterPro; IPR0010100; Pyr redox.

DR InterPro; IPR0010100; Pyr redox.

DR RINTS; PR00411; PURRIASE.

DR PRINTS; PR00411; PURRIASE.

DR RINTS; PR00411; PURRIASEI.

DR TIGRFAMS; TIGRO1316; G1LA; 1.

KW Complete protecome.
             GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0005506; F:electron transport; IEA.
InterPro; IPR000759; Adridx_reductase.
InterPro; IPR001037; FAD_pyr_redox.
InterPro; IPR000501; Halical_ferredxn.
InterPro; IPR000501; Halical_ferredxn.
InterPro; IPR000205; NAD_BS.
InterPro; IPR000103; Pyridine_redox_2.
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA; 50786 MW; 9B29DDBBAE97643A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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60.0%; Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                           Pfam; PF00070; Pyr redox; 1.
PRINTS; PR00353; 4FE45REDOXIN.
PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00368; PADPRN.
PRINTS; PR00469; PNDRDTASEII.
TIGRFAMS; TIGR01316; GltA; 1.
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HSSP; Q28943; 1GTE
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Best Local Similarity
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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

Chen Y., Xue Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Mang J., Yu J., Yang H.;

"A complete sequence of the T. tengcongensis genome.";

Genome Res. 12:689-700 (2002).

EMBL; AE013026; AAM23842.1; -.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
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PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SEQUENCE 425 AA; 46348 MW; 7237DCE3EFD6912E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=GltD; OrderedLocusNames=TTE0567;
Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 2; Length 425;
Pred. No. 7.5;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                  Alr2308 protein.
OrderedLocusNames=alr2308;
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NADPH-dependent glutamate synthase beta chain and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0006189; F:electron transport; IEA.
InterPro; IPR001450; 4Fe45; ferredoxin.
PF00037; Fer4; 1.
                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                    425 AA
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                                                                                                                                                    PRT;
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Local Similarity 61.5%;
Les 8; Conservative
                                      206 COKVCPESCLGNC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 CPSDCPRPCEKIC 120
1 CPKVCPRECESNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CPKVCPRECESNC 13
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017208; AAR33841.1; -. TIGR; GSU0510; -.
                                                                                                                                                                            EMBL; AE017180; AAR33841.1; -. TIGR; GSU0510; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 302:1967-1969(2003).
                                                                                                                                                Science 302:1967-1969(2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 CGRVCPHPCETHC 215
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Pubmed=14671304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 AA;
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                                                                                                                         environments."
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Q7UZUS;
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X MEDLINE=22882897; PubMed=14500908;
A Mandarmar R., Gross R., Raddard G., Simon J., Lanz C., Klimmek O.,
Baar C., Eppinger M., Raddard G., Simon J., Lanz C., Klimmek O.,
A Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
A Meyer F., Lederer H., Schuster S.C.;
"Complete genome sequence and analysis of Wolinella succinogenes.";
"Complete genome sequence and analysis of Wolinella succinogenes.";
Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
R EMBL; BX571658; CAE09617.1; -.
RO; GO:0015018; P:disulfide oxidoreductase activity; IEA.
RO; GO:0015018; P:dectron transport; IEA.
RITEEPRO; IPR000127; PAL DYZ redox.
R InterPro; IPR0001037; Pyri redox.
R InterPro; PR0001037; Pyri redox.
R Pfam; PF00070; Pyr redox: 1.
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   Gaps
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STRAIS-ROA / ATCC 51573;
PubMeds-14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolinella succinogenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-sfrB; ORFNames-GSU0510;
geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATEDEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 2; Length 649;
Pred. No. 11;
1; Mismatches 4; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0419; ADEXDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00469; PNDRDTASEII.
COMDLETE DETOCHOME; OXIGOREGUCEABE.
SEQUENCE 649 AA; 72557 MW; CCAIE7589E36650D CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fe(III) reductase, beta subunit.
   ;
;
                                                                                                                                                                                                                                                                                649 AA
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2.1.43).
Name=FDHB; OrderedLocusNames=WS0477;
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                                                                                                                                                                                                                                                                                PRT;
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Local Similarity 61.5%;
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacteraceae; Wolinella
                                                                                                                         90 CGRVCPQETQCERNC 104
                                                            1 CPKVCPRE--CESNC 13
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   9; Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
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Q74FUS;
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DD 06-JU
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Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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Last annotation update)
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InterPro; IPR001327; FAD pyr redox.
InterPro; IPR0001051; Helical ferredan.
InterPro; IPR001003; Pyridine redox_2.
InterPro; IPR001100; Pyr redox.
Pfam; PF00070; Pyr redox; 1.
PRINTS; PR00410; ADXRDTASE.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
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PROSITE; PS00119; PA2 ASP; UNKNOWN 1.
SEQUENCE 631 AA; 66824 MW; 55BĀE2FC65C34C17 CRC64;
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61.5%;
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                                                              Query Match
Best Local Similarity 53.0.
7; Conservative
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Best Local Similarity 61...
8; Conservative
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MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

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T "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
T "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
T niche differentiation.";

Mauure 424:1047(2003).

MEDLINE AST2094; CAEZO109:1;

MEDLINE EXST20949; Fielectron transporter activity; IEA.

GO: GO:0005108; P:electron transport; IEA.

DR GO; GO:0005108; P:electron transport; IEA.

InterProc. IPR001450; 4Fe44S_ferredoxin.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00037; Fer4; 1. — PROSTIE; PS00198; 4FE45 FERREDOXIN; 1. 4FE-45; Complete proteome; Hypothetical protein; Iron; Iron-sulfur; Ametal-binding.
                                                                                                                                                             Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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EMBL; AB025624; BAB02467.1; -.
GO; GO:0005199; F:structural constituent of cell wall; IEA.
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Pred. No. 8.5;
0; Mismatches 5; Indels
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   (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similarity to late embryogenesis abundant protein.
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InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR009646; Root_cap.
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MEDLINE=20277480; PubMed=10819329;
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PRINTS; PR01218; PSTLEXTENSIN.
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Hypothetical protein.
OrderedLocusNames=PMM1560;
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nes 8; Conservative
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      01-OCT-2003
                                       01-OCT-2003
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STRAIN=ATCC 35405 / DSM 14222;

SURAIN=ATCC 35405 / DSM 14222;

Submad=1506439; DOI=10.1073/pnas.0307639101;

Submad=1506439; DOI=10.1073/pnas.0307639101;

Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,

Burkin S.A., Daugherty S.C., Shetty S. Shvartsbeyn A.,

Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,

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Weinstcock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

"Comparison of the genome of the oral pathogen Treponema denticola
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAY-2004 (TrEMBLrel. 27, Last annotation update)
94-MAY-2004 (TrEMBLrel. 27)
Pyridine nucleotide-disulphide oxidoreductase family protein.
                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Pyridine nucleotide-disulphide oxidoreductase family protein.
Treponema Approximates TDE2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome; Iron; Iron-sulfur; Metal-binding.
Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 914;
                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with other spirochete genomes.";
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
EMBL; AE017253; AAS12687.1; -.
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
Score 52; DB 2
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   914 AA.
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR0010327; FAD_pyr_redox.
InterPro; IPR001013; Pyridine_redox_2.
Pfam; PP00017; Fer4; 2.
Pfam; PP00017; Pyr_redox; 1.
PRINTS; PR00187; Pyr_redox; 1.
PRINTS; PR00181; AFR4SFRDOXIN.
PRINTS; PR00469; PADPNR.
PROSITE; PR00198; 4FR4S_FERREDOXIN; 1.
PROSITE; PR00198; 4FR4S_FERREDOXIN; 1.
4Fe-45; Complete proteome; Iron; Iron-sull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR000759; Adrndx_reductase.
                                                                                                                                                                                                                                                                                                                PRT;
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  61.9%;
53.8%;
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PRT;

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PRELIMINARY;
                          Q7MTD4
 RESULT 15
Q7MTD4
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                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5405 / DSM 14222;

STRAIN=ATCC 35405 / DSM 14222;

Submid=15064399;

A Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

Bodson R.J., Davidsen T.M., Madupu R., Kolonay J., Durkin S.A.,

Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregeorgis E., Geer K.,

T segaye G., Malek J.A., Ayodelj B., Shatsman S., McLeod M.P.,

Smajs D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z.,

Xiang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J.,

R. Praser C.M., Paulsen I.T.;

"Comparison of the genome of the oral pathogen Treponema denticola

with other spirochete genomes.";

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

R. FIGR; TDE2167;
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=PCC 7942;
MEDLINE=22450571; PubMed=12562813;
Katayama M., Kondo T., Xiong J., Golden S.S.;
"lighA encodes an iron-sulfur protein involved in light-dependent modulation of the circadian period in the cyanobacterium Synechococcus elongatus PCC 7942.";
                                                                                                                                                                                                                                                                                                                        Gaps
Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
VCBI_TaxID=158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBL_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Length 352;
Pred. No. 12;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                           Score 52; DB 2; Length 914;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                      914 AA; 101880 MW; 22E32CA9726D4FBE CRC64;
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PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SEQUENCE 352 AA; 37865 MW; 33614612158F2936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:1415-1422 (2003).

EMBL; AY136759; AAN06910.1; -.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:000518; P:electron binding; IEA.

InterPro; IPR001450; 4Fe48_ferredoxin.

Pfam; PF00037; Fer4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%;
                                                                                                                                                                                                                                                                                              61.9%;
61.5%;
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Best Local Similarity 61.50.
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light dependent period
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                 Query Match
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Q8GLI4;
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Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.B., Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;

"Complete genome sequence of the oral pathogenic bacterium Porphyromonas singivalis strain W83.";
J. Bacteriol. 185.5591-5601 (2003).

EMBL, AE017179; AAQ66999.1;
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glutamate synthase, small subunit.
Names-glut, OrderedLocusNames-E962033.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO, GO:0015036; F:disulfide oxidoreductase activity; IEA. GO; GO:006118; P:electron transport; IEA. Interpro; IPR000759; Adrndx reductase.
Interpro; IPR000759; Adrndx reductase.
Interpro; IPR0060137; FAD pyr redox.
Interpro; IPR006004; Glut synth NADFH.
Interpro; IPR00103; Pyridine redox_2.
Interpro; IPR001100; Pyridine redox_2.
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PRINTS; PR004119; PNDEDTASEI.
PRINTS; PR00469; PNDEDTASEII.
PRINTS; PR00469; PNDEDTASEII.
PROSITE; PS00584; PFKB_KINASES_2; UNKNOWN_1.
COMDITE; PROCECOME.
SEQUENCE 462 AA; 49811 MW; 66B2E434EFE7A42E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 51; DB 2; 60.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                     Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
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Best Local Similarity bure
9; Conservative
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=W83;
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Search completed: November 16, 2004, 14:29:48 Job time: 79.5094 secs

CPTDCPRPCERVC 109